```
a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt 49
  Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
                                       10
                                                                   97
gat toa toa cag ggt tot gaa tat gac tat gtc ata ttc aca caa act
Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
                                 25
            20
act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc
Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt
                                                                  193
Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
                        55
tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg
                                                                  241
Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
                    70
                                         75
                                                                  289
gct aca tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt
Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
                                     90
aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc
                                                                  337
Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
                                                     110
            100
                                 105
                                                                  385
gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc
Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
        115
                            120
                                                                  433
ata cca aaq qac atq acc tac cqt aqa ctc atc tct atq atq qqt ttc
Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
                        135
aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc
                                                                  481
Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
145
                                         155
                    150
                                                                  529
gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag
Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
                165
                                     170
                                                                  577
ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag
Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
                                 185
cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat
                                                                  625
Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
        195
                            200
                                                 205
                                                                  646
gtt gac act gaa aat aac cta
Val Asp Thr Glu Asn Asn Leu
    210
                        215
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FIG. 1

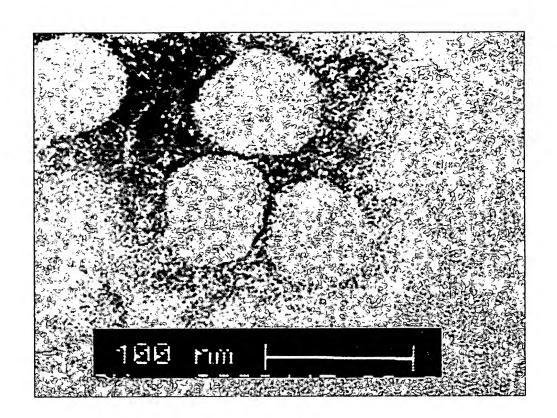


FIG. 2



FIG. 3

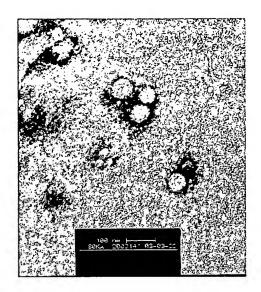


FIG. 4

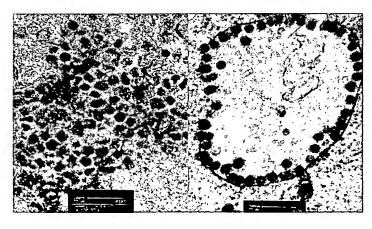


FIG. 5A

FIG. 5B

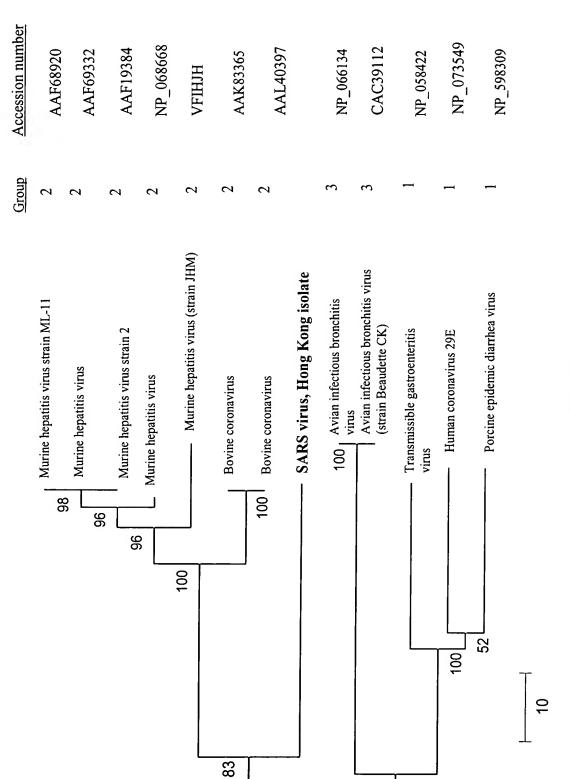


FIG. 6

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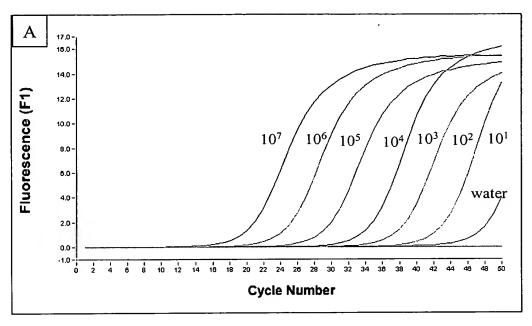


FIG. 7A

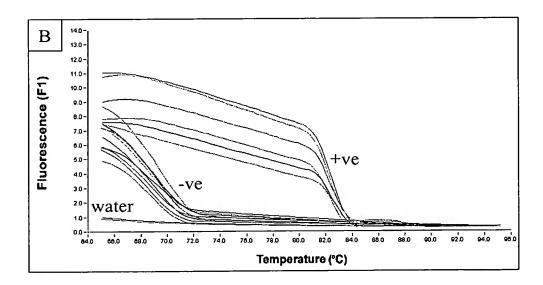


FIG. 7B

t aa Ly 1	aa to ys C <u>y</u>	gt ag vs Se	gt ag er Ar	ga at gg Il 5	c at le Il	a co .e Pr	et go o Al	eg eg La Ar	gt go gg Al 10	la Ar	gc gt cg Va	a ga al Gl	ag to Lu Cy	gt tt ys Ph 15	t gat ne Asp	49
	ttc Phe															97
	gca Ala															145
	atg Met 50															193
	aaa Lys															241
cgc Arg	aca Thr	ttg Leu	ctg Leu	act Thr 85	aaa Lys	ggc Gly	aca Thr	cta Leu	gaa Glu 90	cca Pro	gaa Glu	tat Tyr	ttt Phe	aat Asn 95	tca Ser	289
	tgc Cys															337
	cgc Arg															385
	gac Asp 130															433
	atg Met															481
	aga Arg															529
	tgg Trp			gct					cct					aac		577
	gct Ala															625
	ggt Gly															673

				aat Asn										721
				ttg Leu 245										769
				agt Ser										817
	_	_		gta Val				_	-	_	_	_		865
				cct Pro										913
		_		gaa Glu		_	-	_					_	961
				cgt Arg 325										1009
				ggt Gly										1057
				cgt Arg										1105
				gct Ala										1153
				aac Asn										1201
gaa	aat	aac	cta		(Glu i	Asn i	Asn :	Leu					1213

FIG. 8 Con't

С											et A					tt gct eu Ala 5	49
												cgt Arg					97
gc Al	ct .a	aac Asn	gag Glu 35	tgt Cys	gcg Ala	caa Gln	gta Val	tta Leu 40	agt Ser	gag Glu	atg Met	gtc Val	atg Met 45	tgt Cys	ggc Gly	ggc Gly	145
												ggt Gly 60					193
gc A] 65	La	tat Tyr	gct Ala	aat Asn	agt Ser	gtc Val 70	ttt Phe	aac Asn	att Ile	tgt Cys	caa Gln 75	gct Ala	gtt Val	aca Thr	gcc Ala	aat Asn 80	241
												ata Ile					289
												ctc Leu					337
ga As	at sp	gtt Val	gat Asp 115	cat His	gaa Glu	ttc Phe	gtg Val	gat Asp 120	gag Glu	ttt Phe	tac Tyr	gct Ala	tac Tyr 125	ctg Leu	cgt Arg	aaa Lys	385
												gtt Val 140					433
	er											att Ile					481
												tct Ser	Glu				529
												gaa Glu					577
			_		_				_	-		gtg Val		_			625
												ttt Phe 220					673
Vá			-	-	_	cac His 230		tga	ttg	aaa	ggt	tcc	gtg	tca	ctg	gct	721
a t	- +-	~~+	~~														729

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9841 tatttcagtg gagccttaga tactaccagc tatcgtgaag cagcttgctg ccacttagca
9901 aaggetetaa atgaetttag caacteaggt getgatgtte tetaceaace accacagaca
9961 tcaatcactt ctgctgttct gcagagtggt tttaggaaaa tggcattccc gtcaggcaaa
10021 gttgaagggt gcatggtaca agtaacctgt ggaactacaa ctcttaatgg attgtggttg
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10081 gatgacacag tatactgtcc aagacatgtc atttgcacag cagaagacat gcttaatcct
10141 aactatgaag atctgctcat tcgcaaatcc aaccatagct ttcttgttca ggctggcaat
10201 gttcaacttc gtgttattgg ccattctatg caaaattgtc tgcttaggct taaagttgat
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10381 aatcatacca ttaaaggttc tttccttaat ggatcatgtg gtagtgttgg ttttaacatt
10441 gattatgatt gcgtgtcttt ctgctatatg catcatatgg agcttccaac aggagtacac
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10561 gctgcaggta cagacacaac cataacatta aatgttttgg catggctgta tgctgctgtt
10621 atcaatggtg ataggtggtt tcttaataga ttcaccacta ctttgaatga ctttaacctt
10681 gtggcaatga agtacaacta tgaacctttg acacaagatc atgttgacat attgggacct
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13321 tggaaaggtt atggctgtag ttgtgaccaa ctccgcgaac ccttgatgca gtctgcggat
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FIG. 10 Con't

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13441 caqqcactaq tactqatqtc qtctacaggg cttttgatat ttacaacgaa aaaagtgctg
13501 qttttqcaaa qttcctaaaa actaattqct qtcqcttcca qqaqaaqqat qaggaaggca
13561 atttattaga ctcttacttt gtagttaaga ggcatactat gtctaactac caacatgaag
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13681 ttagagtaga tggtgacatg gtaccacata tatcacgtca gcgtctaact aaatacacaa
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13861 acttcgtaga gaatcctgac atcttacgcg tatatgctaa cttaggtgag cgtgtacgcc
13921 aatcattatt aaagactgta caattctgcg atgctatgcg tgatgcaggc attgtaggcg
13981 tactgacatt agataatcag gatcttaatg ggaactggta cgatttcggt gatttcgtac
14041 aagtagcacc aggctgcgga gttcctattg tggattcata ttactcattg ctgatgccca
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14821 atggtggctg tattaatgcc aaccaagtaa tcgttaacaa tctggataaa tcagctggtt
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16681 ctagaccacc attgaacaga aactatgtct ttactggtta ccgtgtaact aaaaatagta
16741 aagtacagat tggagagtac acctttgaaa aaggtgacta tggtgatgct gttgtgtaca
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FIG. 10 Con't

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16801 gaggtactac gacatacaag ttgaatgttg gtgattactt tgtgttgaca tctcacactg
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16921 tqtacccaac actcaacatc tcagatgagt tttctagcaa tgttgcaaat tatcaaaagg
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17041 ccatcggact tgctctctat tacccatctg ctcgcatagt gtatacggca tgctctcatg
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	aaacaggttc					
	agataataaa					
	atgctgaaat					
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	gtaggcttat					
	actaaacgaa					
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	gtaattttaa					
	ataagggcta					
	aacctatttt					
	ccttttcacc					
	taaagccaac					
	attgttctca					
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29641 ctgcctatat ggaagagccc taatgtgtaa aattaatttt agtagtgcta tccccatgtg
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FIG. 10 Con't

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1 - ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCTCGATCTCTTGTAGATCTGTT - 60
  -ILGFYLPRKSQPTSISCRS V
    Y * V F T Y P G K A N Q P R S L V D L F
     IRFLPTQEKPTNLDLL*ICS
61 - CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC - 120
  -L * T N F K I C V A V A R L H A * C T Y
  - S K R T L K S V * L S L G C M P S A P T
    LNEL*NLCSCRSAACLVHLR
121 - GCAGTATAAACAATAATATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT - 180
  - A V * T I I N F T V V D K K R V T R P S
  - Q Y K Q * * I L L S L T R N E * L V P L
     S I N N N K F Y C R * Q E T S N S S L F
181 - TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC - 240
  -SADCLRFRPCCSRSSAYLGF
  - L Q T A Y G F V R V A V D H Q H T * V S
     C R L L T V S S V L Q S I I S I P R F R
241 - GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA - 300
  -V R V * P K G K M E S L V L G V N E K T
  - S G C D R K V R W R A L F L V S T R K H
     PGVTER*DGEPCSWCQRENT
301 - CACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGG - 360
  - H V Q L S L P V L Q V R D V L V R G F G
  - T S N S V C L S F R L E T C * C V A S G
    R P T Q F A C P S G * R R A S A W L R G
361 - GACTCTGTGGAAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGT - 420
  -DSVEEALSEAREHLKNGTCG
  – TLWKRPYRRHVNTSKMALVV
    LCGRGPIGGT*TPQKWHLWS
421 - CTAGTAGAGCTGGAAAAAGGCGTACTGCCCCAGCTTGAACAGCCCTATGTGTTCATTAAA - 480
  -LVELEKGVLPOLEOPYVFIK
    * * S W K K A Y C P S L N S P M C S L N
  - SRAGKRRTAPA*TALCVH*T
481 - CGTTCTGATGCCTTAAGCACCAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATG - 540
  -RSDALSTNHGHKVVELVAEM
  - V L M P * A P I T A T R S L S W L Q K W
    F * C L K H Q S R P Q G R * A G C R N G
541 - GACGGCATTCAGTACGGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGC - 600
  -DGIQYGRSGITLGVLVPHVG
  - T A F S T V V A V * H W E Y S C H M W A
    R H S V R S * R Y N T G S T R A T C G R
601 - GAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGAGCCGGT - 660
  -ETPIAYRNVLLRKNGNKGAG
  - K P Q L H T A M F F F V R T V I R E P V
- N P N C I P Q C S S S * E R * * G S R W
661 - GGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGAT - 720
  -G H S Y G I D L K S Y D L G D E L G T D
   VIAMASI * SLMT * VTSLALI
  - S * L W H R S K V L * L R * R A W H * S
721 - CCCATTGAAGATTATGAACAAAACTGGAACACTAAGCATGGCAGTGGTGCACTCCGTGAA - 780
  -PIEDYEQNWNTKHGSGALRE
  - P L K I M N K T G T L S M A V V H S V N
  781 - CTCACTCGTGAGCTCAATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGC - 840
  -L T R E L N G G A V T R Y V D N N F C G
  - S L V S S M E V Q S L A M S T T I S V A
    HS * A Q W R C S H S L C R Q Q F L W P
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841 - CCAGATGGGTACCCTCTTGATTGCATCAAAGATTTTCTCGCACGCGGGGCAAGTCAATG - 900
   - P D G Y P L D C I K D F L A R A G K S M
   - Q M G T L L I A S K I F S H A R A S Q C
      RWVPS * LHQRFSRTRGQVNV
901 - TGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAAGAGAGGTGTCTACTGCTGCCGT - 960
   -CTLSEQLDYIESKRGVYCCR
   - A L F P N N L I T S S R R E V S T A A V
     HSFRTT*LHRVEERCLLLP
961 - GACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCTACGAGCACCAG - 1020
   -DHEHEIAWFTERSDKSYEHQ
     T M S M K L P G S L S A L I R A T S T R
     P * A * N C L V H * A L * * E L R A P D
1021 - ACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG - 1080
   -TPFEIKSAKKFDTFKGECPK
   - H P S K L R V P R N L T L S K G N A Q S
      T L R N * E C Q E I * H F Q R G M P K V
1081 - TTTGTGTTTCCTCTTAACTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAG - 1140
   -FVFPLNSKVKVIQPRVEKKK
    LCFLLTQKSKSFNHVLKRKR
      C V S S * L K S Q S H S T T C * K E K D
1141 - ACTGAGGGTTTCATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGT - 1200
   -TEGFMGRIRSVYPVASPQEC
    L R V S W G V Y A L C T L L H L H R S V
     * G F H G A Y T L C V P C C I S T G V *
1201 - AACAATATGCACTTGTCTACCTTGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAG - 1260
   -NNMHLSTLMKCNHCDEVSWQ
    TICTCLP**NVIIAMKFHGR
     Q Y A L V Y L D E M * S L R * S F M A D
1261 - ACGTGCGACTTTCTGAAAGCCACTTGTGAACATTGTGGCACTGAAAATTTAGTTATTGAA - 1320
   -T C D F L K A T C E H C G T E N L V I E
    RATF * K P L V N I V A L K I * L L K
     V R L S E S H L * T L W H * K F S Y * R
1321 - GGACCTACTACATGTGGGTACCTACCTACTAATGCTGTAGTGAAAATGCCATGTCCTGCC - 1380
   -GPTTCGYLPTNAVVKMPCPA
    D L L H V G T Y L L M L * * K C H V L P
     TYYMWVPTY*CCSENAMSCL
1381 - TGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTGCAGATTATCACAACCACTCAAAC - 1440
   -C Q D P E I G P E H S V A D Y H N H S N
    V K T Q R L D L S I V L Q I I T T T Q T
     S R P R D W T * A * C C R L S Q P L K H
1441 - ATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTTGGAGGCTGTGTTTTGCC - 1500
   -IETRLRKGGRTRCFGGCVFA
    L K L D S A R E V G L D V L E A V C L P
     * N S T P Q G R * D * M F W R L C V C L
1501 - TATGTTGGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGCTGATATTGGC - 1560
   -'Y V G C Y N K R A Y W V P R A S A D I G
    M L A A I I S V P T G F L V L V L I L A C W L L * * A C L L G S S C * C * Y W L
1561 - TCAGGCCATACTGGCATTACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAG - 1620
   -SGHTGITGDNVETLNEDLLE
    Q A I L A L L V T M W R P * M R I S L R R P Y W H Y W * Q C G D L E * G S P * D
-ILS RERVNINIVG D F H L N E E
       * V V N V L T L T L L A I F I * M K R
      TES*TC*H*HCWRFSFE*RG
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1681 - GTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAG - 1740
   -VAIILASFSASTSAFIDTIK
   - L P S F W H L S L L L Q V P L L T L * R
      C H H F G I F L C F Y K C L Y * H Y K E
1741 - AGTCTTGATTACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTATAAAGTTACC - 1800
   -SLDYKSFKTIVESCGNYKVT
   - V L I T S L S K P L L S P A V T I K L P
      S * L Q V F Q N H C * V L R * L * S Y Q
1801 - AAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTAACACCA - 1860
   -KGKPVKGAWNIGQQRSVLTP
   - RESP * K V L G T L D N R D Q F * H H
     G K A R K R C L E H W T T E I S F N T T
1861 - CTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTT - 1920
   -L C G F P S Q A A G V I R S I F A R T L
   - C V V F P H R L L V L S D Q F L R A H L
     V W F S L T G C W C Y Q I N F C A H T *
1921 - GATGCAGCAAACCACTCAATTCCTGATTTGCAAAGAGCAGCTGTCACCATACTTGATGGT - 1980
   -DAANHSIPDLQRAAVTILDG
   - M O O T T Q F L I C K E Q L S P Y L M V
      CSKPLNS*FAKSSCHHT*WY
1981 - ATTTCTGAACAGTCATTACGTCTTGTCGACGCCATGGTTTATACTTCAGACCTGCTCACC - 2040
   -I S E Q S L R L V D A M V Y T S D L L T
   - F L N S H Y V L S T P W F I L Q T C S P
     F * T V I T S C R R H G L Y F R P A H Q
2041 - AACAGTGTCATTATTATGGCATATGTAACTGGTGGTCTTGTACAACAGACTTCTCAGTGG - 2100
   -NSVIIMAYVTGGLVQQTSQW
   - T V S L L W H M * L V V L Y N R L L S G
   - Q C H Y Y G I C N W W S C T T D F S V V
2101 - TTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATCTTTGAATGGATTGAG - 2160
   -LSNLLGTTVEKLRPIFEWIE
    C L I F W A L L L K N S G L S L N G L R
     V * S F G H Y C * K T Q A Y L * M D * G
2161 - GCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATTTCTC - 2220
   -AKLSAGVEFLKDAWEILKFL
    RNLVQELNFSRMLGRFSNFS
     ET*CRS*ISQGCLGDSQISH
2221 - ATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAG - 2280
   -ITGVFDIVKGQIQVASDNIK
    LQVFLTSSRVKYRLLQITSR
     YRCF*HRQGSNTGCFR*HQG
2281 - GATTGTGTAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAA - 2340
   -DCVKCFIDVVNKALEMCIDQ
    IV*NASLMLLTRHSKCALIK
     LCKMLH * CC * QGTRNVH * SS
2341 - GTCACTATCGCTGGCGCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAA - 2400
   -V T I A G A K L R S L N L G E V F I A Q
   - S L S L A Q S C D H S T * V K S S S L K
     HYRWRKVAITQLR*SLHRSK
2401 - AGCAAGGGACTTTACCGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACTACTCATGCCT - 2460
   -SKGLYRQCIRGKEQLQLLMP
-ARDFTVSVYVARSSCNYSCL
     Q G T L P S V Y T W Q G A A A T T H A S
2461 - CTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATTCACATGACACAGTACTTACC - 2520
   - L K A P K E V T F L E G D S H D T V L T
- L R H Q K K * P F L K V I H M T Q Y L P
     * G T K R S N L S * R * F T * H S T Y L
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2521 - TCTGAGGAGGTTGTTCTCAAGAACGGTGAACTCGAAGCACTCGAGACGCCCGTTGATAGC - 2580
   -SEEVVLKNGELEALETPVDS
   - L R R L F S R T V N S K H S R P L I A
     * G G C S O E R * T R S T R D A R * * L
2581 - TTCACAAATGGAGCTATCGTCGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAG - 2640
   -FTNGAIVGTPVCVNGLMLLE
   - S Q M E L S S A H Q S V * M A S C S * R
     H K W S Y R R H T S L C K W P H A L R D
-I K D K E Q Y C A L S P G L L A T N N V
   - L R T K N N T A H C L L V Y W L Q T M S
     * G Q R T I L R I V S W F T G Y K Q C L
2701 - TTTCGCTTAAAAGGGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGG - 2760
   -FRLKGGAPIKGVTFGEDTVW
   - FA * KG V H Q L K V * P L E K I L F G
     S L K R G C T N * R C N L W R R Y C L G
2761 - GAAGTTCAAGGTTACAAGAATGTGAGAATCACATTTGAGCTTGATGAACGTGTTGACAAA - 2820
   -E V Q G Y K N V R I T F E L D E R V D K
   - K F K V T R M * E S H L S L M N V L T K
     S S R L Q E C E N H I * A * * T C * Q S
2821 - GTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGAATCCGGTACCGAAGTTACTGAGTTT - 2880
   -VLNEKCSVYTVESGTEVTEF
   - C L M K S A L S T L L N P V P K L L S L
     A * * K V L C L H C * I R Y R S Y * V C
2881 - GCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTTCTGATCTCCTTACC - 2940
   - A C V V A E A V V K T L Q P V S D L L T
   - H V L * Q R L L * R L Y N Q F L I S L P
     M C C S R G C C E D F T T S F * S P Y Q
2941 - AACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCT - 3000
   -NMGIDLDEWSVATFYLFDDA
   - T W V L I L M S G V * L H S T Y L M M L
     H G Y * S * * V E C S Y I L L I * * C W
3001 - GGTGAAGAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGATGAGGAAGAA - 3060
   -GEENFSSRMYCSFYPPDEEE
    V K K T F H H V C I V P F T L Q M R K K
     * R K L F I T Y V L F L L P S R * G R R
3061 - GAGGACGATGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGT - 3120
   -EDDAECEEEIDETCEHEYG
   - R T M Q S V R K K L M K P V N M S T V
     GRCRV * GRRN * * N L * T * V R Y
3121 - ACAGAGGATGATTATCAAGGTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGA - 3180
   -TEDDYQGLPLEFGASAETVR
   - O R M I I K V S L W N L V P Q L K Q F E
     RG*LSRSPSGIWCLS*NSSS
3181 - GTTGAGGAAGAGAAGAGAGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAG - 3240
   -VEEEEEDWLDDTTEQSEIE
   - L R K K R K T G W M I L L S N Q R L S
     * G R R R G R L A G * Y Y * A I R D * A
3241 - CCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAAACTT - 3300
   -PEPEPTPEEPVNQFTGYLKL
     Q N Q N L H L K N Q L I S L L V I * N L
     RTRTYT*RTS*SVYWLFKTY
3301 - ACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTGCTAATCCT - 3360
   -T D N V A I K C V D I V K E A Q S A N P
    LTMLPLNVLTSLRRHKVLIL
      * O C C H * M C * H R * G G T K C * S Y
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3361 - ATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCA - 3420
   - M V I V N A A N I H L K H G G G V A G A
     W * L * M L L T Y T * N M V V V * Q V H
      G D C K C C * H T P E T W W W C S R C T
3421 - CTCAACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAAT - 3480
   -LNKATNGAMQKESDDYIKLN
   - S T R Q P M V P C K R R V M I T L S * M
      Q Q G N Q W C H A K G E * * L H * A K W
3481 - GGCCCTCTTACAGTAGGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGT - 3540
   -GPLTVGGSCLLSGHNLAKKC
   - A L L Q * E G L V C F L D I I L L R S V
     PSYSRRVLFAFWT*SC*EVS
3541 - CTGCATGTTGTTGGACCTAAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCA - 3600
   -LHVVGPNLNAGEDIQLLKAA
   - C M L L D L T * M Q V R T S S F L R Q H
      ACCWT*PKCR*GHPAS*GSI
3601 - TATGAAAATTTCAATTCACAGGACATCTTACTTGCACCATTGTTGTCAGCAGGCATATTT - 3660
   -YENFNSQDILLAPLLSAGIF
   - M K I S I H R T S Y L H H C C Q Q A Y L
     * K F Q F T G H L T C T I V V S R H I W
3661 - GGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTCGTACACAGGTTTAT - 3720
   -GAKPLQSLQVCVQTVRTQVY
   - V L N H F S L Y K C A C R R F V H R F I
      C * T T S V F T S V R A D G S Y T G L Y
3721 - ATTGCAGTCAATGACAAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACCTG - 3780
   -I A V N D K A L Y E Q V V M D Y L D N L
   - L Q S M T K L F M S R L S W I I L I T *
     C S Q * Q S S L * A G C H G L S * * P E
3781 - AAGCCTAGAGTGGAAGCACCTAAACAAGAGGGGCCACCAAACACAGAAGATTCCAAAACT - 3840
   -KPRVEAPKQEEPPNTEDSKT
   - S L E W K H L N K R S H Q T Q K I P K L
      A * S G S T * T R G A T K H R R F Q N *
3841 - GAGGAGAATCTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATT - 3900
   -EEKSVVQKPVDVKPKIKACI
   - R R N L S Y R S L S M * S Q K L R P A L
     GEICRTEACRCEAKN*GLH*
3901 - GATGAGGTTACCACAACACTGGAAGAAACTAAGTTTCTTACCAATAAGTTACTCTTGTTT - 3960
   -DEVTTTLEETKFLTNKLLLF
   - M R L P Q H W K K L S F L P I S Y S C L
     * G Y H N T G R N * V S Y Q * V T L V C
3961 - GCTGATATCAATGGTAAGCTTTACCATGATTCTCAGAACATGCTTAGAGGTGAAGATATG - 4020
   - A D I N G K L Y H D S Q N M L R G E D M
   - LISMVSFTMILRTCLEVKIC
     * Y O W * A L P * F S E H A * R * R Y V
4021 - TCTTTCCTTGAGAAGGATGCACCTTACATGGTAGGTGATGTTATCACTAGTGGTGATATC - 4080
   -S F L E K D A P Y M V G D V I T S G D I
    LSLRRMHLTW * VMLSLVVIS
     FP*EGCTLHGR*CYH*W*YH
4081 - ACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCT - 4140
   -T C V V I P S K K A G G T T E M L S R A
    LVL*YPPKRLVALLRCSQEL
     L C C N T L Q K G W W H Y * D A L K S F
4141 - TTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGT - 4200
   -L K K V P V D E Y I T T Y P G Q G C A G
    * R K C Q L M S I * P R T L D K D V L V
      E E S A S * * V Y N H V P W T R M C W L
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4201 - TATACACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTA - 4260
   -YTLEEAKTALKKCKSAFYVL
   - I H L R K L R L L L R N A N L H F M Y Y
     Y T * G S * D C S * E M Q I C I L C T T
4261 - CCTTCAGAAGCACCTAATGCTAAGGAAGAGATTCTAGGAACTGTATCCTGGAATTTGAGA - 4320
   -PSEAPNAKEEILGTVSWNLR
   - L Q K H L M L R K R F * E L Y P G I * E
     FRST * C * GRD S R N C I L E F E R
4321 - GAAATGCTTGCTCATGCTGAAGAGACAAGAAAATTAATGCCTATATGCATGGATGTTAGA - 4380
   -EMLAHAEETRKLMPICMDVR
   - K C L L M L K R Q E N * C L Y A W M L E
     NACSC*RDKKINAYMHGC*S
4381 - GCCATAATGGCAACCATCCAACGTAAGTATAAAGGAATTAAAATTCAAGAGGGCATCGTT - 4440
   -AIMATIQRKYKGIKIQEGIV
   - P * W Q P S N V S I K E L K F K R A S L
    HNGNHPT * V * RN * N S RG H R *
4441 - GACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACG - 4500
   -DYGVRFFFYTSKEPVASIIT
   - T M V S D S S F I L V K S L * L L L R
    L W C P I L L Y * * R A C S F Y Y Y E
4501 - AAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGGT - 4560
   -KLNSLNEPLVTMPIGYVTHG
   - S * T L * M S R L S Q C Q L V M * H M V
    A E L S K * A A C H N A N W L C D T W F
4561 - TTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTCA - 4620
   -FNLEEAARCMRSLKAPAVVS
   - L I L K R L R A V C V L L K L L P * C Q
     * S * R G C A L Y A F S * S C R S V S
4621 - GTATCATCACCAGATGCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACA - 4680
   - V S S P D A V T T Y N G Y L T S S S K T
   - Y H H Q M L L L H I M D T S L R H Q R H
     IITRCCYYI*WIPHFVIKDI
-SEEHFVETVSLAGSYRDWSY
   - L R S T L * K Q F L W L A L T E I G P I
     * G A L C R N S F F G W L L Q R L V L F
4741 - TCAGGACAGCGTACAGAGTTAGGTGTTGAATTTCTTAAGCGTGGTGACAAAATTGTGTAC - 4800
   -SGQRTELGVEFLKRGDKIVY
   - Q D S V Q S * V L N F L S V V T K L C T
    RTAYRVRC*IS*AW*QNCVP
4801 - CACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGGTTCTTTCACTTGACAAA - 4860
   -HTLESPVEFHLDGEVLSLDK
   - T L W R A P S S F I L T V R F F H L T N
    HSGEPRRVSS*R*GSFT*QT
4861 - CTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACTGTGGAC - 4920
   -LKSLLSLREVKTIKVFTTVD
   - * R V S Y P C G R L R L * K C S Q L W T
    KESLIPAGG*DYKSVHNCGQ
4921 - AACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGT - 4980
   -N T N L H T Q L V D M S M T Y G Q Q F G
   - TLISTHSLWICL* HMDSSLV
   - H * S P H T A C G Y V Y D I W T A V W S
4981 - CCAACATACTTGGATGGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGT - 5040
   -PTYLDGADVTKIKPHVNHEG
   - Q H T W M V L M L Q K L N L M * I M R V
   - N I L G W C * C Y K N * T S C K S * G *
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5041 - AAGACTTTCTTTGTACTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTAC - 5100
   -KTFFVLPSDDTLRSEAFEYY
   - R L S L Y Y L V M T H Y V V K L S S T T
     D F L C T T * * * H T T * * S F R V L P
5101 - CATACTCTTGATGAGAGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCACACAAAGAAA - 5160
   -HTLDESFLGRYMSALNHTKK
   - I L L M R V F L V G T C L L * T T Q R N
     YS * * E F S W * V H V C F K P H K E M
5161 - TGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAAATGGGCTGATAACAATTGTTAT - 5220
   -WKFPQVGGLTSIKWADNNCY
   - GNFLKLVV * LQLNGLITIVI
   - EISSSWWFNFN * MG * * QLLF
5221 - TTGTCTAGTGTTTTATTAGCACTTCAACAGCTTGAAGTCAAATTCAATGCACCAGCACTT - 5280
   -LSSVLLALQQLEVKFNAPAL
   - C L V F Y * H F N S L K S N S M H Q H F
     V * C F I S T S T A * S Q I Q C T S T S
5281 - CAAGAGGCTTATTATAGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTC - 5340
   -QEAYYRARAGDAANFCALIL
   - K R L I I E P V L V M L L T F V H S Y S
     RGLL*SPCW*CC*LLCTHTR
5341 - GCTTACAGTAATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTT - 5400
   -AYSNKTVGELGDVRETMTHL
   - L T V I K L L A S L V M S E K L * P I F - L Q * * N C W R A W * C Q R N Y D P S S
5401 - CTACAGCATGCTAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGT - 5460
   -LQHANLESAKRVLNVVCKHC
   - Y S M L I W N L Q S E F L M W C V N I V
     TAC * FGICKASS * CGV * TLW
5461 - GGTCAGAAAACTACTACCTTAACGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCT - 5520
   -GQKTTTLTGVEAVMYMGTLS
   - V R K L L P * R V * K L * C I W V L Y L
   - SENYYLNGCRSCDVYGYSIL
-YDNLKTGVSIPCVCGRDATQ
   - MIILRQVFPFHVCVVMLHN
     * * S * D R C F H S M C V W S * C Y T I
5581 - TATCTAGTACAACAAGAGTCTTCTTTTGTTATGATGTCTGCACCACCTGCTGAGTATAAA - 5640
   -Y L V Q Q E S S F V M M S A P P A E Y K
   - I * Y N K S L L L * C L H H L L S I N
     SSTTRVFFCYDVCTTC*V*I
5641 - TTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCAT - 5700
   -LQQGTFLCANEYTGNYQCGH
   - Y S K V H S Y V R M S T L V T I S V V I
     TARYILMCE * V H W * L S V W S L
5701 - TACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAG - 5760
   -YTHITAKETLYRIDGAHLTK
   - T L I * L L R R P S I V L T E L T L Q R - H S Y N C * G D P L S Y * R S S P Y K D
5761 - ATGTCAGAGTACAAAGGACCAGTGACTGTTTTCTACAAGGAAACATCTTACACTACA - 5820
   - M S E Y K G P V T D V F Y K E T S Y T T - C Q S T K D Q * L M F S T R K H L T L Q
    V R V Q R T S D * C F L Q G N I L H Y N
-TIKPVSYKLDGVTYTEIEPK
   - P S S L C R I N S M E L L T Q R L N Q N
      H Q A C V V * T R W S Y L H R D * T K I
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5881 - TTGGATGGGTATTATAAAAAGGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTA - 5940
   -L D G Y Y K K D N A Y Y T E Q P I D L V
   - W M G I I K R I M L T I Q S S L * T L Y
     GWVL*KG*CLLYRAAYRPCT
5941 - CCAACTCAACCATTACCAAATGCGAGTTTTGATAATTTCAAACTCACATGTTCTAACACA - 6000
   -PTQPLPNASFDNFKLTCSNT
   - Q L N H Y Q M R V L I I S N S H V L T Q
     N S T I T K C E F * * F Q T H M F * H K
6001 - AAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTCACGAGAGCTA - 6060
   -KFADDLNQMTGFTKPASREL
   - N L L M I * I K * Q A S Q S Q L H E S Y
      I C * * F K S N D R L H K A S F T R A I
6061 - TCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTAT - 6120
   -SVTFFPDLNGDVVAIDYRHY
   - L S H S S Q T * M A M * W L L T I D T I
      CHILPRLEWRCSGY*L*TLF
6121 - TCAGCGAGTTTCAAGAAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAAC - 6180
   -SASFKKGAKLLHKPIVWHIN
   - Q R V S R K V L N Y C I S Q L F G T L T
      SEFQERC*ITA*ANCLAH*P
6181 - CAGGCTACAACCAAGACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGT - 6240
   -QATTKTTFKPNTWCLRCLWS
     R L Q P R Q R S N Q T L G V Y V V F G V
     G Y N Q D N V Q T K H L V F T L S L E Y
6241 - ACAAAGCCAGTAGATACTTCAAATTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGA - 6300
   -TKPVDTSNSFEVLAVEDTQG
   - Q S Q * I L Q I H L K F W Q * K T H K E
     KASRYFKFI * SSGSRRHTRN
6301 - ATGGACAATCTTGCTTGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGTGGAAAATCCT - 6360
   - M D N L A C E S Q Q P T S E E V V E N P
   - W T I L L V K V N N P P L K K * W K I L
     GQSCL*KSTTHL*RSSGKSY
6361 - ACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTACCGAAGTTGTAGGCAATGTC - 6420
   -TIQKEVIECDVKTTEVVGNV
   - P Y R R K S * S V T * K L P K L * A M S
     HTEGSHRV * RENYRSCRQCH
6421 - ATACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGATCTT - 6480
   -I L K P S D E G V K V T Q E L G H E D L
   - Y L N H Q M K V L K * H K S * V M R I L
     T * T I R * R C * S N T R V R S * G S Y
6481 - ATGGCTGCTTATGTGGAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTA - 6540
   - M A A Y V E N T S I T I K K P N E L S L
   - W L L M W K T Q A L P L R N L M S F H *
   - G C L C G K H K H Y H * E T * * A F T S
6541 - GCCTTAGGTTTAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGG - 6600
   -ALGLKTIATHGIAAINSVPW
   - P * V * K Q L P L M V L L Q L I V F L G
    LRFKNNCHSWYCCN**CSLE
6601 - AGTAAAATTTTGGCTTATGTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAAT - 6660
   -SKILAYVKPFLGQAAITTSN
   - V K F W L M S N H S * D K Q Q L Q H Q I
   - * N F G L C Q T I L R T S S N Y N I K L
6661 - TGCGCTAAGAGATTAGCACAACGTGTGTTTAACAATTATATGCCTTATGTGTTTACATTA - 6720
   -CAKRLAQRVFNNYMPYVFTL
     A L R D * H N V C L T I I C L M C L H Y
      R * E I S T T C V * Q L Y A L C V Y I I
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6721 - TTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTAGAATTAGAGCTTCACTACCT - 6780
   -LFQLCTFTKSTNSRIRASLP
   - C S N C V L L L K V P I L E L E L H Y L
     V P I V Y F Y * K Y Q F * N * S F T T Y
6781 - ACAACTATTGCTAAAAATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGATGCCGGCATT - 6840
   -TTIAKNSVKSVAKLCLDAGI
   - Q L L L K I V L R V L L N Y V W M P A L
     N Y C * K * C * E C C * I M F G C R H *
6841 - AATTATGTGAAGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTG - 6900
   -NYVKSPKFSKLFTIAMWLLL
   - I M * S H P N F L N C S Q S L C G Y C C
     LCEVTQIF * I V H N R Y V A I V V
6901 - TTAAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTTGGTGTACTCTTATCT - 6960
   -L S I C L`G S L I C V T A A F G V L L S
    * V F A * V L * S V * L L L V Y S Y L
    KYLLRFSNLCNCCFWCTLI*
6961 - AATTTTGGTGCTCCTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAAC - 7020
   -NFGAPSYCNGVRELYLNSSN
   - I L V L L I V M A L E N C I L I R L T
    FWCSFLL*WR*RIVS*FV*R
7021 - GTTACTACTATGGATTTCTGTGAAGGTTCTTTTCCTTGCAGCATTTGTTTAAGTGGATTA - 7080
   -V T T M D F C E G S F P C S I C L S G L
   - L L L W I S V K V L F L A A F V * V D *
   - YYYGFL*RFFSLQHLFKWIR
7081 - GACTCCCTTGATTCTTATCCAGCTCTTGAAACCATTCAGGTGACGATTTCATCGTACAAG - 7140
   -DSLDSYPALETIQVTISSYK
   - T P L I L I Q L L K P F R * R F H R T S
    LP*FLSSS*NHSGDDFIVQA
7141 - CTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTCACA - 7200
   -LDLTILGLAAEWVLAYMLFT
    * T * Q F * V W P L S G F W H I C C S Q
     R L D N F R S G R * V G F G I Y V V H K
7201 - AAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTTGCT - 7260
   -KFFYLLGLSAIMQVFFGYFA
   - N S F I Y * V F Q L * C R C S L A I L L
    ILLFIRSFSYNAGVLWLFC*
7261 - AGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCA - 7320
   -SHFISNSWLMWFIISIVQMA
   - V I S S A I L G S C G L S L V L Y K W H
   - S F H Q Q F L A H V V Y H * Y C T N G T
-PVSAMVRMYIFFASFYYIWK
   - P F L Q W L G C T S S L L L S T T Y G R
    R F C N G * D V H L L C F F L L H M E E
7381 - AGCTATGTTCATATCATGGATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGC - 7440
   -SYVHIMDGCTSSTCMMCYKR
   - A M F I S W M V A P L R L A * C A I S A
    LCSYHGWLHLFDLHDVL*AQ
7441 - AATCGTGCCACACGCGTTGAGTGTACAACTATTGTTAATGGCATGAAGAGATCTTTCTAT - 7500
   -NRATRVECTTIVNGMKRSFY
   - I V P H A L S V Q L L L M A * R D L S M
    SCHTR*VYNYC*WHEEIFLC
7501 - GTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAATTGGAATTGTCTCAATTGT - 7560
   -VYANGGRGFCKTHNWNCLNC
   - S M Q M E A V A S A R L T I G I V S I V
     LCKWRPWLLQDSQLELSQL*
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7561 - GACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAGTTGCTCGTGATTTGTCACTC - 7620
   -DTFCTGSTFISDEVARDLSL
   - T H F A L V V H S L V M K L L V I C H S
     H I L H W * Y I H * * * S C S * F V T P
7621 - CAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTTGCT - 7680
   -QFKRPINPTDQSSYIVDSVA
     SLKDQSTLLTSHRILLIVLL
     V * K T N Q P Y * P V I V Y C * * C C C
7681 - GTGAAAATGGCGCGCTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGA - 7740
   -V K N G A L H L Y F D K A G Q K T Y E R
    * K M A R F T S T L T R L V K R P M R D
     EKWRASPLL * QGWSKDL * ET
7741 - CATCCGCTCTCCCATTTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCA - 7800
   - H P L S H F V N L D N L R A N N T K G S
   - I R S P I L S I * T I * E L T T L K V H
     S A L P F C Q F R Q F E S * Q H * R F T
7801 - CTGCCTATTAATGTCATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAG - 7860
   -LPINVIVFDGKSKCDESASK
   - C L L M S * F L·M A S P N A T S L L L S
     A Y * C H S F * W Q V Q M R R V C F * V
7861 - TCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAACCTATTCTGTTGCTTGACCAAGCT - 7920
   -SASVYYSQLMCQPILLLDQA
   - L L L C T T V S * C A N L F C C L T K L
     C F C V L Q S A D V P T Y S V A * P S S
7921 - CTTGTATCAAACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTTTGATGCTTATGTC - 7980
   -L V S N V G D S T E V S V K M F D A Y V
   - LYQTLEIVLKFPLRCLMLMS
     C I K R W R * Y * S F R * D V * C L C R
7981 - GACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTACA - 8040
   -DTFSATFSVPMEKLKALVAT
   - T P F O O L L V F L W K N L R H L L L Q
      H L F S N F * C S Y G K T * G T C C Y S
8041 - GCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCA - 8100
   -AHSELAKGVALDGVLSTFVS
    LTAS*QRV*L*MVSFLHSCQ
      SQRVSKGCSFRWCPFYIRVS
8101 - GCTGCCCGACAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTC - 8160
   - A A R Q G V V D T D V D T K D V I E C L
    L P D K V L L I P M L T Q R M L L N V S
      C P T R C C * Y R C * H K G C Y * M S Q
8161 - AAACTTTCACATCACTCTGACTTAGAAGTGACAGGTGACAGTTGTAACAATTTCATGCTC - 8220
   -KLSHHSDLEVTGDSCNNFML
   - N F H I T L T * K * Q V T V V T I S C S
      TFTSL*LRSDR*OL*OFHAH
8221 - ACCTATAATAAGGTTGAAAACATGACGCCCAGAGATCTTGGCGCATGTATTGACTGTAAT - 8280
   -TYNKVENMTPRDLGACIDCN
    PIIRLKT * RPEILAHVLTVM
     L * * G * K H D A Q R S W R M Y * L * C
8281 - GCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTA - 8340
   -ARHINAQVAKSHNVSLIWNV
    QGISMPK * QKVTMFHSSGM *
      K A Y Q C P S S K K S Q C F T H L E C K
8341 - AAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTACTGCTGCCAAGAAG - 8400
   -KDYMSLSEQLRKQIRTAAKK
   - K T T C L Y L N S C V N K F V L L P R R
      R L H V F I * T A A * T N S Y C C O E E
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8401 - AACAACATACCTTTTACACTAACTTGTGCTACAACTAGACAGGTTGTCAATGTCATAACT - 8460
   -NNIPFTLTCATTRQVVNVIT
   - T T Y L L H * L V L Q L D R L S M S * L - Q H T F Y T N L C Y N * T G C Q C H N Y
8461 - ACTAAAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAG - 8520
   -TKISLKGGKIVSTCFKLMLK
   - L K S H S R V V R L L V L V L N L C L R
      * N L T Q G W * D C * Y L F * T Y A * G
-ATLLCVLAALVCYIVMPVHT
   - P H Y C A F L L H W F V I S L C Q Y I H
      H I I V R S C C I G L L Y R Y A S T Y I
8581 - TTGTCAATCCATGATGGTTACACAAATGAAATCATTGGTTACAAAGCCATTCAGGATGGT - 8640
   -L S I H D G Y T N E I I G Y K A I Q D G
   - C Q S M M V T Q M K S L V T K P F R M V
      V N P * W L H K * N H W L Q S H S G W C
8641 - GTCACTCGTGACATCATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGAC - 8700
   -V T R D I I S T D D C F A N K H A G F D
   - S L V T S F L L M I V L Q I N M L V L T
      H S * H H F Y * * L F C K * T C W F * R
8701 - GCATGGTTTAGCCAGCGTGGTGGTTCATACAAAATGACAAAAGCTGCCCTGTAGTAGCT - 8760
   - A W F S Q R G G S Y K N D K S C P V V A
   - H G L A S V V V H T K M T K A A L * * L
      \texttt{M} \ \ \texttt{V} \ \ \ \texttt{P} \ \ \texttt{A} \ \ \texttt{W} \ \ \ \texttt{F} \ \ \texttt{I} \ \ \texttt{Q} \ \ \texttt{K} \ \ \texttt{L} \ \ \texttt{P} \ \ \texttt{C} \ \ \texttt{S} \ \ \texttt{C}
8761 - GCTATCATTACAAGAGAGATTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAGA - 8820
   -AIITREIGFIVPGLPGTVLR
    - L S L Q E R L V S * C L A Y R V L C * E
      Y H Y K R D W F H S A W L T G Y C A E S
8821 - GCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTTGGCAACATT - 8880
    -AING D F L H F L P R V F S A V G N I
    - Q S M V T S C I F Y L V F L V L L A T F
      N Q W * L L A F S T S C F * C C W Q H L
8881 - TGCTACACACCTTCCAAACTCATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCTT - 8940
    -CYTPSKLIEYSDFATSACVL
    - A T H L P N S L S I V I L L P L L A F L
     LHTFQTH*V**FCYLCLRSC
8941 - GCTGCTGAGTGTACAATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGAC - 9000
    - A A E C T I F K D A M G K P V P Y C Y D
    - L L S V Q F L R M L W A N L C H I V M T
      C * V Y N F * G C Y G Q T C A I L L * H
9001 - ACTAATTTGCTAGAGGGTTCTATTTCTTATAGTGAGCTTCGTCCAGACACTCGTTATGTG - 9060
    -TNLLEGSISYSELRPDTRYV
    - LIC * R V L F L I V S F V Q T L V M C
      * FARGFYFL * * ASSRHSLCA
9061 - CTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACCTGGAGGGTTCTGTTAGAGTA - 9120
    -L M D G S I I Q F P N T Y L E G S V R V
    - L W M V P S Y S F L T L T W R V L L E *
      YGWFHHTVS*HLPGGFC*SS
9121 - GTAACAACTTTTGATGCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAAGTAGGT - 9180
    -V T T F D A E Y C R H G T C E R S E V G
        Q L L M L S T V D M V H A K G Q K * V
       NNF * C * V L * T W Y M R K V R S R Y
9181 - ATTTGCCTATCTACCAGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCA - 9240
    -ICLSTSGRWVLNNEHYRALS
    - FAYLPVVDGFLIMSITELYQ
      L P I Y Q W * M G S * * * A L Q S S I R
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9241 - GGAGTTTTCTGTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTG - 9300
    -G V F C G V D A M N L I A N I F T P L V
    - E F S V V L M R * I S * L T S L L L C
       S F L W C * C D E S H S * H L Y S S C A
9301 - CAACCTGTGGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATA - 9360
    -QPVGALDVSASVVAGGIIAI
      N L W V L * M C L L Q * W L V V L L P Y
       T C G C F R C V C F S S G W W Y Y C H I
9361 - TTGGTGACTTGTGCTGCCTACTTTTATGAAATTCAGACGTGTTTTTGGTGAGTACAAC - 9420
    -L V T C A A Y Y F M K F R R V F G E Y N
    - W * L V L P T T L * N S D V F L V S T T
       G D L C C L L Y E I Q T C F W * V Q P
- H V V A A N A L L F L M S F T I L C L V
    - M L L L M H F C F * C L S L Y S V W Y
        \texttt{C} \ \texttt{C} \ \texttt{C} \ \texttt{C} \ \texttt{C} \ \texttt{T} \ \texttt{F} \ \texttt{V} \ \texttt{F} \ \texttt{D} \ \texttt{V} \ \texttt{F} \ \texttt{H} \ \texttt{Y} \ \texttt{T} \ \texttt{L} \ \texttt{S} \ \texttt{G} \ \texttt{T} 
9481 - CCAGCTTACAGCTTTCTGCCGGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTAT - 9540
    -PAYSFLPGVYSVFYLYLTFY
    - Q L T A F C R E S T Q S F T C T * H S I
      S L Q L S A G S L L S L L L V L D I L F
9541 - TTCACCAATGATGTTTCATTCTTGGCTCACCTTCAATGGTTTTGCCATGTTTTCTCCTATT - 9600
    -FTNDVSFLAHLQWFAMFSPI
    - S P M M F H S W L T F N G L P C F L L L
      HQ * C F I L G S P S M V C H V F S Y C
9601 - GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGG - 9660
    -V P F W I T A I Y V F C I S L K H C H W
    - C L F G * Q Q S M Y S V F L * S T A I G
      A F L D N S N L C I L Y F S E A L P L V
9661 - TTCTTTAACAACTATCTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTC - 9720
    -FFNNYLRKRVMFNGVTFSTF
     SLTTILGKESCLMELHLVPS
      L * O L S * E K S H V * W S Y I * Y L R
9721 - GAGGAGGCTGCTTTGTGTACCTTTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGC - 9780
    -EEAALCTFLLNKEMYLKLRS
     R R L L C V P F C S T R K C T * N C V A
       G G C F V Y L F A Q Q G N V P K I A * R
9781 - GAGACACTGTTGCCACTTACACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAG - 9840
    -ETLLPLTQYNRYLALYNKYK
    - R H C C H L H S I T G I L L Y I T S T S
      D T V A T Y T V * Q V S C S I * Q V Q V
9841 - TATTTCAGTGGAGCCTTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCA - 9900
    -Y F S G A L D T T S Y R E A A C C H L A
     I S V E P * I L P A I V K Q L A A T * Q
F Q W S L R Y Y Q L S * S S L L P L S K
-KALNDFSNSGADVLYQPPQT
     RL * M T L A T Q V L M F S T N H H R H
      GSK*L*QLRC*CSLPTTTDI
9961 - TCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTTAGGAAAATGGCATTCCCGTCAGGCAAA - 10020
    -SITSAVLQSGFRKMAFPSGK
     Q S L L L F C R V V L G K W H S R Q A K
      N H F C C S A E W F * E N G I P V R Q S
10021 - GTTGAAGGGTGCATGGTACAAGTAACCTGTGGAACTACAACTCTTAATGGATTGTGGTTG - 10080
    -VEGCMVQVTCGTTTLNGLWL
-LKGAWYK*PVELQLLMDCGW
       * R V H G T S N L W N Y N S * W I V V G
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10081 - GATGACACAGTATACTGTCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCT - 10140
    - D D T V Y C P R H V I C T A E D M L N P
    * H S I L S K T C H L H S R R H A * S
10141 - AACTATGAAGATCTGCTCATTCGCAAATCCAACCATAGCTTTCTTGTTCAGGCTGGCAAT - 10200
    -NYEDLLIRKSNHSFLVQAGN
    - T M K I C S F A N P T I A F L F R L A M
     L·* R S A H S Q I Q P * L S C S G W Q C
10201 - GTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCTTAAAGTTGAT - 10260
    - V Q L R V I G H S M Q N C L L R L K V D
    - FNFVLLAILCKIVCLGLKLI
      STSCYWPFYAKLSA*A*S*Y
10261 - ACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTATCCAACCTGGTCAAACATTT - 10320
    -TSNPKTPKYKFVRIQPGQTF
    - L L T L R H P S I N L S V S N L V K H F
      F * P * D T O V * I C P Y P T W S N I F
10321 - TCAGTTCTAGCATGCTACAATGGTTCACCATCTGGTGTTTATCAGTGTGCCATGAGACCT - 10380
    -SVLACYNGSPSGVYQCAMRP
    - O F * H A T M V H H L V F I S V P * D L
     SSSMLQWFTIWCLSVCHET*
10381 - AATCATACCATTAAAGGTTCTTTCCTTAATGGATCATGTGGTAGTGTTTGATTTAACATT - 10440
    -NHTIKGSFLNGSCGSVGFNI
    - I I P L K V L S L M D H V V V L V L T L
     SYH * RFFP * WIMW * CWF * H *
10441 - GATTATGATTGCGTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACAC - 10500
    - D Y D C V S F C Y M H H M E L P T G V H
    - I M I A C L S A I C I I W S F Q Q E Y T
     L * L R V F L L Y A S Y G A S N R S T R
-AGTDLEGKFYGPFVDRQTAQ
    - L V L T * K V N S M V H L L T D K L H R
     WY*LRR*ILWSIC*QTNCTG
10561 - GCTGCAGGTACAGACAACCATAACATTAAATGTTTTGGCATGGCTGTATGCTGCTGTT - 10620
    - A A G T D T T I T L N V L A W L Y A A V
     LQVQTQP*H*MFWHGCMLLL
     C R Y R H N H N I K C F G M A V C C C Y
10621 - ATCAATGGTGATAGGTGGTTTCTTAATAGATTCACCACTACTTTGAATGACTTTAACCTT - 10680
    -ING D R W F L N R F T T L N D F N L
    - S M V I G G F L I D S P L L * M T L T L - Q W * * V V S * * I H H Y F E * L * P C
10681 - GTGGCAATGAAGTACAACTATGAACCTTTGACACAAGATCATGTTGACATATTGGGACCT - 10740
    -VAMKYNYEPLTQDHVDILGP
    - w Q * s T T M N L * H K I M L T Y W D L
    - GNEVQL * TFDTRSC * HIGTS
10741 - CTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTG - 10800
    -LSAQTGIAVLDMCAALKELL
    - F L L K Q E L P S * I C V L L * K S C C
     F C S N R N C R L R Y V C C F E R A A A
10801 - CAGAATGGTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACA - 10860
    -QNGMNGRTILGSTILEDEFT
    - R M V * M V V L S L V A L F * K M S L H
     E W Y E W S Y Y P W * H Y F R R * V Y T
10861 - CCATTTGATGTTGTTAGACAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATT - 10920
    - P F D V V R Q C S G V T F Q G K F K K I
     H L M L L D N A L V L P S K V S S R K L
      I * C C * T M L W C Y L P R * V Q E N C
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10921 - GTTAAGGGCACTCATCATTGGATGCTTTTAACTTTCTTGACATCACTATTGATTCTTGTT - 10980
    -V K G T H H W M L L T F L T S L L I L V
    - L R A L I I G C F * L S * H H Y * F L F
      * G H S S L D A F N F L D I T I D S C S
10981 - CAAAGTACACAGTGGTCACTGTTTTTTTTTTTTCGAGAATGCTTTCTTGCCATTTACT - 11040
    - O S T Q W S L F F F V Y E N A F L P F T
    - K V H S G H C F S L F T R M L S C H L L
      K Y T V V T V F L C L R E C F L A I Y S
11041 - CTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTC - 11100
    -LGIMAIAACAMLLVKHKHAF
    - L V L W Q L L H V L C C L L S I S T H S
      W Y Y G N C C M C Y A A C * A * A R I L
11101 - TTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATATGGTCTACATG - 11160
    -LCLFLLPSLATVAYFNMVYM
    - C A C F C Y L L L Q Q L L T L I W S T C
      V L V S V T F S C N S C L L * Y G L H A
11161 - CCTGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCT - 11220
    -PASWVMRIMTWLELADTSLS
    - L L A G * C V S * H G L N W L T L A C L
      C * L G D A Y H D M A * I G * H * L V W
11221 - GGTTATAGGCTTAAGGATTGTGTTATGTTATGCTTCAGCTTTAGTTTTGCTTATTCTCATG - 11280
    -GYRLKDCVMYASALVLIILM
    - VIGLRIVLCMLQL * FCLFS *
      L * A * G L C Y V C F S F S F A Y S H D
11281 - ACAGCTCGCACTGTTTATGATGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATT - 11340
    -TARTVYDDAARRVWTLMNVI
    - Q L A L F M M M L L D V F G H * * M S L
      SSHCL**CC*TCLDTDECHY
11341 - ACACTTGTTTACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCC - 11400
    -TLVYKVYYGNALDQAISMWA
    - H L F T K S T M V M L * I K L F P C G P
      TCLQSLLW * CFRSSYFH V G L
11401 - TTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTATCATGTTTTTAGCT - 11460
    -L V I S V T S N Y S G V V T T I M F L A
     * L F L * P L T I L V S L R L S C F * L
      SYFCNL * LFWCRYDYHVFS *
-RAIVFVCVEYYPLLFITGNT
-EL*CLCVLSITHCYLLATP
      S Y S V C V C * V L P I V I Y Y W Q H L
11521 - TTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGC - 11580
    -L Q C I M L V Y C F L G Y C C C Y F G
    - Y S V S C L F I V S * A I V A A A T L A
      T V Y H A C L L F L R L L L L L W P
11581 - CTTTTCTGTTTACTCAACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTC - 11640
    -L F C L L N R Y F R L T L G V Y D Y L V
     F S V Y S T V T S G L L L V F M T T W S
      F L F T Q P L L Q A Y S W C L * L L G L
11641 - TCTACACAAGAATTTAGGTATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATT - 11700
    -STQEFRYMNSQGLLPPKSSI
     L H K N L G I * T P R G F C L L R V V L
      YTRI*VYELPGAFAS*E*Y*
11701 - GATGCTTTCAAGCTTAACATTAAGTTGTTGGGGTATTGGAGGTAAACCATGTATCAAGGTT - 11760
    -DAFKLNIKLLGIGGKPCIKV
    - M L S S L T L S C W V L E V N H V S R L
      C F Q A * H * V V G Y W R * T M Y Q G C
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11761 - GCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACATCTGTGGTACTGCTCTCGGTT - 11820
    -ATVQSKMSDVKCTSVVLLSV
    - L L Y S L K C L T * S A H L W Y C S R F
      Y C T V * N V * R K V H I C G T A L G S
11821 - CTTCAACAACTTAGAGTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTACAACTCCAC - 11880
    -LQQLRVESSSKLWAQCVQLH
    - F N N L E * S H L L N C G H N V Y N S T
       STT * SR V I F * I V G T M C T T P Q
11881 - AATGATATTCTTCTTGCAAAAGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTG - 11940.
    -NDILLAKDTTEAFEKMVSLL
    - M I F F L Q K T Q L K L S R R W F L F C
       * Y S S C K R H N * S F R E D G F S F V
11941 - TCTGTTTTGCTATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTC - 12000
    -S V L L S M Q G A V D I N R L C E E M L
    - L F C Y P C R V L * T L I G C A R K C S
       C F A I H A G C C R H * * V V R G N A R
12001 - GATAACCGTGCTACTCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCC - 12060
    -DNRATLQAIASEFSSLPSYA
    - I T V L L F R L L L Q N L V L Y H H M P
       * P C Y S S G Y C F R I * F F T I I C R
12061 - GCTTATGCCACTGCCCAGGAGGCCTATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTC - 12120
    - A Y A T A Q E A Y E Q A V A N G D S E V
    - L M P L P R R P M S R L * L M V I L K S
      LCHCPGGL*AGCS*W*F*SR
12121 - GTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCTAAATCTGAGTTTTGACCGTGATGCT - 12180
    -V L K K L K K S L N V A K S E F D R D A
    - F S K S * R N L * M W L N L S L T V M L
      S Q K V K E I F E C G * I * V * P * C C
12181 - GCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAG - 12240
    - A M Q R K L E K M A D Q A M T Q M Y K Q
    - P C N A S W K R W Q I R L * P K C T N R
      HATQVGKDGRSGYDPNVQTG
12241 - GCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCACT - 12300
    - A R S E D K R A K V T S A M Q T M L F T
    - Q D L R T R G Q K * L V L C K Q C S S L
      KI * G Q E G K S N * C Y A N N A L H Y
12301 - ATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGT - 12360
    -M L R K L D N D A L N N I I N N A R D G
    - C L G S L I M M H L T T L S T M R V M V - A * E A * * * C T * Q H Y Q Q C A * W L
12361 - TGTGTTCCACTCAACATCATACCATTGACTACAGCAGCCCAAACTCATGGTTGTTGTCCCT - 12420
    -C V P L N I I P L T T A A K L M V V V P
    - V F H S T S Y H * L Q Q P N S W L L S L
    - CSTQHHTIDYSSQTHGCCP*
12421 - GATTATGGTACCTACAAGAACACTTGTGATGGTAACACCTTTACATATGCATCTGCACTC - 12480
    -DYGTYKNTCDGNTFTYASAL
    - I M V P T R T L V M V T P L H M H L H S
      LWYLQEHL*W*HLYICICTL
12481 - TGGGAAATCCAGCAAGTTGTTGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAAC - 12540
    -WEIQQVVDADSKIVQLSEIN
     - G K S S K L L M R I A R L F N L V K L T
       G N P A S C * C G * Q D C S T * * N * H
12541 - ATGGACAATTCACCAAATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACTCA - 12600
     - M D N S P N L A W P L I V T A L R A N S
     W T I H Q I W L G L L L Q L * E P T Q
       G Q F T K F G L A S Y C Y S S K S Q L S
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12601 - GCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTCCTGTGCG - 12660
    -AVKLQNNELSPVALRQMSCA
    - L L N Y R I M N * V Q * H Y D R C P V R
      C * T T E * * T E S S S T T T D V L C G
12661 - GCTGGTACCACACAAACAGCTTGTACTGATGACAATGCACTTGCCTACTATAACAATTCG - 12720
    -AGTTQTACTDDNALAYYNNS
    - L V P H K Q L V L M T M H L P T I T I R
      W Y H T N S L Y * * Q C T C L L * Q F E
12721 - AAGGGAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGA - 12780
    -KGGRFVLALLSDHQDLKWAR
    - REVGLCWHYYQTTKISNGLD
      GR*VCAGITIRPPRSQMG*I
12781 - TTCCCTAAGAGTGATGGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTT - 12840
    -FPKSDGTGTIYTELEPPCRF
    - S L R V M V Q V Q F T Q N W N H L V G L
       P * E * W Y R Y N L H R T G T T L * V C
12841 - GTTACAGACACACAAAAGGGCCTAAAGTGAAATACTTGTACTTCATCAAAGGCTTAAAC - 12900
    -V T D T P K G P K V K Y L Y F I K G L N
    - L O T H O K G L K * N T C T S S K A * T
      YRHTKRA*SEILVLHQRLKQ
12901 - AACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCTTCAGGCTGGA - 12960
    -NLNRGMVLGSLAATVRLQAG
    - T * I E V W C W A V * L L Q Y V F R L E
      PK * RYGAGQFSCYSTSSGWK
12961 - AATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCTTCTGTGCTTTTGCAGTAGAC - 13020
    -NATEVPANSTVLSFCAFAVD
    - M L Q K Y L P I Q L C F P S V L L Q * T
      CYRSTCQFNCAFLLCFCSRP
13021 - CCTGCTAAAGCATATAAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGTG - 13080
    -PAKAYKDYLASGGQPITNCV
    - L L K H I R I T * Q V E D N Q S P T V *
      C * S I * G L P S K W R T T N H Q L C E
13081 - AAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAAC - 13140
    -KMLCTHTGTGQAITVTPEAN
    - R C C V H T L V Q D R Q L L * H Q K L T
      13141 - ATGGACCAAGAGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGAC - 13200
    - M D Q E S F G G A S C C L Y C R C H I D
    - W T K S P L V V L H V V C I V D A T L T - G P R V L W W C F M L S V L * M P H * P
- H P N P K G F C D L K G K Y V Q I P T T
    - I Q I L K D S V T * K V S T S K Y L P L - S K S * R I L * L E R * V R P N T Y H L
13261 - TGTGCTAATGACCCAGTGGGTTTTACACTTAGAAACACAGTCTGTACCGTCTGCGGAATG - 13320
    -CANDPVGFTLRNTVCTVCGM
    - V L M T Q W V L H L E T Q S V P S A E C
      C * * P S G F Y T * K H S L Y R L R N V
13321 - TGGAAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCCTTGATGCAGTCTGCGGAT - 13380
    -W K G Y G C S C D Q L R E P L M Q S A D
    - G K V M A V V V T N S A N P * C S L R M - E R L W L * L * P T P R T L D A V C G C
13381 - GCATCAACGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCA - 13440
    - A S T F L N G F A V * V Q P V L H R A A
    - H Q R F * T G L R C K C S P S Y T V R H
       I N V F K R V C G V S A A R L T P C G T
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13441 - CAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAAGTGCTG - 13500
    -QALVLMSSTGLLIFTTKKVL
    - R H * Y * C R L Q G F * Y L Q R K K C W
      G T S T D V V Y R A F D I Y N E K S A G
13501 - GTTTTGCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCA - 13560
    -VLQSS*KLIAVASRRMRKA
    - F C K V P K N * L L S L P G E G * G R Q
      F A K F L K T N C C R F Q E K D E E G N
13561 - ATTTATTAGACTCTTACTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAG - 13620
    -IY*TLTL*LRGILCLTTNMK
    - FIRLLLCS * EAYYV * LPT * R
      L L D S Y F V V K R H T M S N Y Q H E E
13621 - AGACTATTTATAACTTGGTTAAAGATTGTCCAGCGGTTGCTGTCCATGACTTTTTCAAGT - 13680
    -RLFITWLKIVQRLLSMTFSS
    - D Y L * L G * R L S S G C C P * L F Q V
      TIYNLVKDCPAVAVHDFFKF
-LE * M V T W Y H I Y H V S V * L N T Q
    - * S R W * H G T T Y I T S A S N * I H N
      R V D G D M V P H I S R Q R L T K Y T M
13741 - TGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGATACATTAAAAG - 13800
    -WLI*SMLYVILMRVIVIH*K
    - G * F S L C S T S F * * G * L * Y I K R
      A D L V Y A L R H F D E G N C D T L K E
13801 - AAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATG - 13860
    -KYSSHTIAVMMIISIRRIGM
    - N T R H I Q L L * * * L F Q * E G L V *
     ILVTYNCCDDDYFNKKDWYD
13861 - ACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCC - 13920
    -T S * R I L T S Y A Y M L T * V S V Y A
    - L R R E S * H L T R I C * L R * A C T P
      F V E N P D I L R V Y A N L G E R V R Q
13921 - AATCATTATTAAAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCG - 13980
    -NHY*RLYNSAMLCVMQAL*A
    - I I I K D C T I L R C Y A * C R H C R R
      S L L K T V Q F C D A M R D A G I V G V
13981 - TACTGACATTAGATAATCAGGATCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTAC - 14040
    -y * H * I I R I L M G T G T I S V I S Y
    - T D I R * S G S * W E L V R F R * F R T
     L T L D N Q D L N G N W Y D F G D F V Q
14041 - AAGTAGCACCAGGCTGCGGAGTTCCTATTGTGGATTCATATTACTCATTGCTGATGCCCA - 14100
    -K * H Q A A E F L L W I H I T H C * C P
    - S S T R L R S S Y C G F I L L I A D A H
      V A P G C G V P I V D S Y Y S L L M P I
14101 - TCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGATGCTGATCTCGCAAAAC - 14160
    -SSL * LG H W L L S P I W M L I S Q N
    - P H F D * G I G C * V P Y G C * S R K T
     LTLTRALAAESHMDADLAKP
14161 - CACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGACTTTGTCTCTCG - 14220
    - H L L S G I C * N M I L R K R D F V S S
    - T Y * V G F A E I * F Y G R E T L S L R
     LIKWDLLKYDFTEERLCLFD
14221 - ACCGTTATTTTAAATATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATG - 14280
    -TVILNIGTRHTIPIVLTVWM
     PLF * ILGPDIPSQLY * LFG *
      R Y F K Y W D Q T Y H P N C I N C L D D
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14281 - ATAGGTGTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTA - 14340
    -I G V S F I V Q T L M C Y F L L C F H L
     * V Y P S L C K L * C V I F Y C V S T Y
      RCILHCANFNVLFSTVFPPT
14341 - CAAGTTTTGGACCACTAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTTCAA - 14400
    -Q V L D H * * E K Y L * M V F L L L F Q
      K F W T T S K K N I C R W C S F C C F N
      S F G P L V R K I F V D G V P F V V S T
14401 - CTGGATACCATTTTCGTGAGTTAGGAGTCGTACATAATCAGGATGTAAACTTACATAGCT - 14460
    -LDTIFVS*ESYIIRM*TYIA
    - W I P F S * V R S R T * S G C K L T * L
      G Y H F R E L G V V H N Q D V N L H S S
-RVSVSRNF * CMLLIQLCMQL
    - A S Q F Q G T F S V C C * S S Y A C S F
      R L S F K E L L V Y A A D P A M H A A S
-LAIYC * INALHAFQ * LH * Q T
    - W O F I A R * T H Y M L F S S C T N K Q
      G N L L L D K R T T C F S V A A L T N N
14581 - ATGTTGCTTTTCAAACTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTG - 14640
    -M L L F K L S N P V I L I K T F M T L L
    - C C F S N C Q T R * F * * R L L * L C C
      V A F Q T V K P G N F N K D F Y D F A V
14641 - TGTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTC - 14700
    -CLKVSLRKEVLLN*NTSSLL
    - V * R F L * G R K F C * T K T L L C S
      S K G F F K E G S S V E L K H F F F A Q
14701 - AGGATGGCAACGCTGCTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGT - 14760
    -RMATLLSVIMTIIVIICQQC
    - G W Q R C Y Q * L * L L S L * S A N N V
      D G N A A I S D Y D Y Y R Y N L P T M C
14761 - GTGATATCAGACACTCCTATTCGTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACG - 14820
    -VISDNSYS * LKLLINTLIVT
     * Y Q T T P I R S * S C * * I L * L L R
      DIRQLLFVVEVVDKYFDCYD
14821 - ATGGTGGCTGTATTAATGCCAACCAAGTAATCGTTAACAATCTGGATAAATCAGCTGGTT - 14880
    -MVAVLMPTK * SLTIWINQLV
    - W W L Y * C Q P S N R * Q S G * I S W F
      G G C I N A N Q V I V N N L D K S A G F
14881 - TCCCATTTAATAATGGGGTAAGGCTAGACTTTATTATGACTCAATGAGTTATGAGGATC - 14940
    -SHLING V RLD FIMTQ * V M R I
     PI * * M G * G * T L L * L N E L * G S
      P F N K W G K A R L Y Y D S M S Y E D Q
14941 - AAGATGCACTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATC - 15000
    - K M H F S R I L S V M S S L L * L K * I
     RCTFRVY*A*CHPYYNSNES
      DALFAYTKRNVIPTITQMNL
15001 - TTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTA - 15060
    - L S M P L V Q R I E L A P * L V S L S V - * V C H * C K E * S S H R S W C L Y L *
      K Y A I S A K N R A R T V A G V S I C S
15061 - GTACTATGACAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG - 15120
    - V L * Q I D S F I R N Y * S Q * P P L E
- Y Y D K * T V S S E I I E V N S R H * R
      T M T N R Q F H Q K L L K S I A A T R G
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-ELLW*LEQASFTVAGIIC*K
    - S Y C G N W N K Q V L R W L A * Y V K N
     A T V V I G T S K F Y G G W H N M L K T
15181 - CTGTTTACAGTGATGTAGAAACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACA - 15240
    -L F T V M * K L H T L W V G I I Q N V T
    - C L Q * C R N S T P Y G L G L S K M * Q
      V Y S D V E T P H L M G W D Y P K C D R
15241 - GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA - 15300
    -EPCLTCLG * WPLLFLLANIT
    AMPNMLRIMASLVLARKHNT
15301 - CTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA - 15360
    -LAVTYHTVSTG * LTSVRKY *
    - L L * L I T P F L Q V S * R V C A S I K
      C C N L S H R F Y R L A N E C A Q V L S
15361 - GTGAGATGGTCATGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTG - 15420
    - V R W S C V A A H Y M L N Q V E H H P V
    - * D G H V. W R L T I C * T R W N I I R *
     E M V M C G G S L Y V K P G G T S S G D
15421 - ATGCTACAACTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATG - 15480
    -M L Q L L M L I V S L T F V K L L Q P M
    - C Y N C L C * * C L * H L S S C Y S Q C
     ATTAYANS V F N I C Q A V T A N V
15481 - TAAATGCACTTCTTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC - 15540
    - * M H F F Q L M V I R * L T S M S A I Y
    - K C T S F N * W * * D S * Q V C P Q S T
     N A L L S T D G N K I A D K Y V R N L Q
15541 - AACACAGGCTCTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG - 15600
    -N T G S M S V S I E I G M L I M N S W M
    - T O A L * V S L * K * G C * S * I R G *
     H R L Y E C L Y R N R D V D H E F V D E
15601 - AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATCTTTCTGATGATGCCGTTG - 15660
    -SFTLTCVNISP**FFLMMPL
    - V L R L P A * T F L H D D S F * * C R C
     F Y A Y L R K H F S M M I L S D D A V V
-CAITVTMRLKV**LALRTLR
    - V L * Q * L C G S R F S S * H * E L * G
     CYNSNYAAQGLVASIKNFKA
15721 - CAGTTCTTTATTATCAAAATAATGTGTTCATGTCTGAGGCAAAATGTTGGACTGAGACTG - 15780
    -QFFIIKIMCSCLRQNVGLRL
    - S S L L S K * C V H V * G K M L D * D *
     V L Y Y Q N N V F M S E A K C W T E T D
15781 - ACCTTACTAAAGGACCTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAG - 15840
    -TLLKDLTNFAHSIQC * LNKE
    - P Y * R T S R I L L T A Y N A S * T R R
     LTKGPHEFCSQHTMLVKQGD
15841 - ATGATTACGTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTG - 15900
    -MITCTCLTQIHQEY*AQAVL
     * L R V P A L P R S I K N I R R R L F C
      D Y V Y L P Y P D P S R I L G A G C F V
15901 - TCGATGATATTGTCAAAACAGATGGTACACTTATGATTGAAAGGTTCGTGTCACTGGCTA - 15960
    -SMILSKQMVHL * LKGSCHWL
     R * Y C Q N R W Y T Y D * K V R V T G Y
     D D I V K T D G T L M I E R F V S L A I
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15961 - TTGATGCTTACCCACTTACAAAACATCCTAATCAGGAGTATGCTGATGTCTTTCACTTGT - 16020
    -LMLTHLQNILIRSMLMSFTC
     * C L P T Y K T S * S G V C * C L S L V
      DAYPLTKHPNQEYADVFHLY
16021 - ATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGCCACATGTTGGACATGTATT - 16080
    -I Y N T L E S Y M M S L L A T C W T C I
    - F T I H * K V T * * A Y W P H V G H V F
      LQYIRKLHDELTGHMLDMYS
16081 - CCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTATGAGGCTA - 16140
    -P * C * L M I T P H G T G N L S F M R L
    - R N A N * * * H L T V L G T * V L * G Y
      V M L T N D N T S R Y W E P E F Y E A M
16141 - TGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGA - 16200
    -CTHHIQSCRL*VLVYCAIHR
    - V H T T Y S L A G C R C L C I V Q F T D
    - Y T P H T V L Q A V G A C V L C N S Q T
16201 - CTTCACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAGTGCTGCTATG - 16260
    -L H F V A V P V L G D H S Y V A S A A M
    - FTSLRCLY * ETIPMLQ V L L *
      S L R C G A C I R R P F L C C K C C Y D
16261 - ACCATGTCATTTCAACATCACAAATTAGTGTTGTCTGTTAATCCCTATGTTTGCAATG - 16320
    -TMSFQHHTN*CCLLIPMFAM
    - P C H F N I T Q I S V V C * S L C L Q C
      H V I S T S H K L V L S V N P Y V C N A
16321 - CCCCAGGTTGTGATGTCACTGATGTGACACACTGTATCTAGGAGGTATGAGCTATTATT - 16380
    -PQVVMSLM*HNCI*EV*AII
    - P R L * C H * C D T T V S R R Y E L L L
      PGCDVTDVTQLYLGGMSYYC
16381 - GCAAGTCACATAAGCCTCCCATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTT - 16440
    -ASHISLPLVFHYVLMVRFLV
    - O V T * A S H * F S I M C * W S G F W F
    - KSHKPPISFPLCANGQVFGL
16441 - TATACAAAAACACATGTGTAGGCAGTGACAATGTCACTGACTTCAATGCGATAGCAACAT - 16500
    - Y T K T H V * A V T M S L T S M R * Q H
    - I Q K H M C R Q * Q C H * L Q C D S N M
      YKNTCVGSDNVTDFNAIATC
16501 - GTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAAGC - 16560
    -VIGLMLAITYLPTLVLRDSS
    - * L D * C W R L H T C Q H L Y * E T Q A
      D W T N A G D Y I L A N T C T E R L K L
16561 - TTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTG - 16620
    -FSQQKRSKPLRKHLSCHMVL
    - FRSRNAQSH * GNI * AVIWYC
      F A A E T L K A T E E T F K L S Y G I A
16621 - CCACTGTACGCGAAGTACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAAC - 16680
    -PLYAKYSLTENCIFHGRLEN
    - H C T R S T L * Q R I A S F M G G W K T
      T V R E V L S D R E L H L S W E V G K P
16681 - CTAGACCACCATTGAACAGAAACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTA - 16740
    -L D H H * T E T M S L L V T V * L K I V
    - * T T I E Q K L C L Y W L P C N * K *
      R P P L N R N Y V F T G Y R V T K N S K
16741 - AAGTACAGATTGGAGAGTACACCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTGTACA - 16800
    -KYRLESTPLKKVTMVMLLCT
    · S T D W R V H L * K R * L W * C C C V Q
      V O I G E Y T F E K G D Y G D A V V Y R
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16801 - GAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTGTGTTGACATCTCACACTG - 16860
    -EVLRHTS * MLVITLC * HLTL
    - R Y Y D I Q V E C W * L L C V D I S H C
      G T T T Y K L N V G D Y F V L T S H T V
16861 - TAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATTACTGGCT - 16920
    - * C H L V H L L * C H K S T M * E L L A
    - NAT * CTYSSATRALCENYW L
       M P L S A P T L V P Q E H Y V R I T G L
16921 - TGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGG - 16980
    -CTQHSTSQMSFLAMLQIIKR
    - V P N T Q H L R * V F * Q C C K L S K G
       Y P T L N I S D E F S S N V A N Y Q K V
16981 - TCGGCATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTG - 17040
    -SACKSTLHSKDHLVLVRVIL
    - R H A K V L Y T P R T T W Y W * E S F C
       G M Q K Y S T L Q G P P G T G K S H F A
17041 - CCATCGGACTTGCTCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATG - 17100
    -PSDLLSITHLLA*CIRHALM
    - H R T C S L L P I C S H S V Y G M L S C
       I G L A L Y Y P S A R I V Y T A C S H A
17101 - CAGCTGTTGATGCCCTATGTGAAAAGGCATTAAAATATTTGCCCATAGATAAATGTAGTA - 17160
    -Q L L M P Y V K R H * N I C P * I N V V
     SC * C P M * K G I K I F A H R * M *
       A V D A L C E K A L K Y L P I D K C S R
17161 - GAATCATACCTGCGCGTGCGCGTAGAGTGTTTTGATAAATTCAAAGTGAATTCAACAC - 17220
    -ESYLRVRA*SVLINSK*IQH
    - N H T C A C A R R V F * * I Q S E F N T
      I I P A R A R V E C F D K F K V N S T L
17221 - TAGAACAGTATGTTTTCTGCACTGTAAATGCATTGCCAGAAACAACTGCTGACATTGTAG - 17280
    - * N S M F S A L * M H C Q K Q L L T L *
    - R T V C F L H C K C I A R N N C * H C S
      EQYVFCTVNALPETTADIVV
17281 - TCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTC - 17340
    -SLMKSLWLLIMT * VLSMLDF
    - L * * N L Y G Y * L * L E C C Q C * T S
      F D E I S M A T N Y D L S V V N A R L R
17341 - GTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCGCACATTGC - 17400
    -V Q N T T S I L A I L L N Y Q P P A H C
    - C K T L R L Y W R S C S I T S P P H I A
      AKHYVYIGDPAQLPAPRTLL
17401 - TGACTAAAGGCACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAA - 17460
    - * L K A H * N Q N I L I Q C A D L * K Q
    - D * R H T R T R I F * F S V Q T Y E N N
    - TKGTLEPEYFNSVCRLMKTI
17461 - TAGGTCCAGACATGTTCCTTGGAACTTGTCGCCGTTGTCCTGCAAATTGTTGACACTG - 17520
    - * V Q T C S L E L V A V V L L K L L T L
    - R S R H V P W N L S P L S C * N C * H C
      G P D M F L G T C R R C P A E I V D T V
17521 - TGAGTGCTTTAGTTTATGACAATAAGCTAAAAGCACACAAGGATAAGTCAGCTCAATGCT - 17580
    - * V L * F M T I S * K H T R I S Q L N A
- E C F S L * Q * A K S T Q G * V S S M L
      S A L V Y D N K L K A H K D K S A Q C F
17581 - TCAAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATCTGCAATCAACAGACCTC - 17640
    -S K C S T K V L L H M M F H L Q S T D L
     Q N V L Q R C Y Y T * C F I C N Q Q T S
       K M F Y K G V I T H D V S S A I N R P O
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17641 - AAATAGGCGTTGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTA - 17700
    -K * A L * E N F L H A I L L G E K L F L
    - N R R C K R I S Y T Q S C L E K S C F Y
      I G V V R E F L T R N P A W R K A V F I
17701 - TCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGA - 17760
    -SHLIIHRTL*LQKS*DCLRR
    - L T L * F T E R C S F K N L R I A Y A D
      S P Y N S Q N A V A S K I L G L P T Q T
17761 - CTGTTGATTCATCACAGGGTTCTGAATATGACTATGTCATATTCACACAAACTACTGAAA - 17820
    -LLIHHRVLNMTMSYSHKLLK
    - C * F I T G F * I * L C H I H T N Y * N
      V D S S Q G S E Y D Y V I F T Q T T E T
17821 - CAGCACACTCTTGTAATGTCAACCGCTTCAATGTGGCTATCACAAGGGCAAAAATTGGCA - 17880
    -QHTLVMSTASMWLSQGQKLA
    - S T L L * C Q P L Q C G Y H K G K N W H
      A H S C N V N R F N V A I T R A K I G I
17881 - TTTTGTGCATAATGTCTGATAGAGATCTTTATGACAAACTGCAATTTACAAGTCTAGAAA - 17940
    -FCA * CLIEIFM TNCNLQV * K
    - F V H N V * * R S L * Q T A I Y K S R N
      L C I M S D R D L Y D K L Q F T S L E I
17941 - TACCACGTCGCAATGTGGCTACATTACAAGCAGAAAATGTAACTGGACTTTTTAAGGACT - 18000
    -YHVAMWLHYKQKM*LDFLRT
    - TTSQCGYITSRKCNWTF * G L
      PRRNVATLQAENVTGLFKDC
18001 - GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA - 18060
    -V V R S L L V F I L H R H L H T S A L I
       * D H Y W S S S Y T G T Y T P Q R * Y
      S K I I T G L H P T Q A P T H L S V D I
18061 - TAAAATTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT - 18120
    - * N S R L K D Y V L T Y Q A Y Q R T * P
    - KIOD*RIMC*HTRHTKGHDL
      K F K T E G L C V D I P G I P K D M T Y
18121 - ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTA - 18180
    -T V D S S L * W V S K * I T K S M V T L
     P * T H L Y D G F Q N E L P S Q W L P *
R R L I S M M G F K M N Y Q V N G Y P N
-ICLSPAKKLFVTFVRGLALM
     Y V Y H P R R S Y S S R S C V D W L * C
      M F I T R E E A I R H V R A W I G F D V
- * R A V M Q L E M L W V L T Y L S S * D
    - R G L S C N * R C C G Y * P T S P A R I
      EGCHATRDAVGTNLPLQLGF
18301 - TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA - 18360
    -FLQVLT * * LYRLVMLTLKIT
    - FYRC * LSSCTDWLC * H * K * H
      S T G V N L V A V P T G Y V D T E N N T
18361 - CAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATAC - 18420
    - Q N S P E L M Q N L H Q V T S L N I L Y - R I H Q S * C K T S T R * P V * T S Y T
      E F T R V N A K P P P G D Q F K H L I P
18421 - CACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCA - 18480
    - H S C I K A C P G M * C V L R * Y K C S
     THV * RLALECSAY * DSTNAQ
      LMYKGLPWNVVRIKIVOMLS
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18481 - GTGATACACTGAAAGGATTGTCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTG - 18540
    -VIH * K D C Q T E S C S S F G R M A L
     * Y T E R I V R Q S R V R P L G A W L *
      D T L K G L S D R V V F V L W A H G F E
18541 - AGCTTACATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTG - 18600
    -SLHQ*STLSRLDLKERVVCV
    - A Y I N E V L C Q D W T * K N V L S V *
      LTSMKYFVKIGPERTCCLCD
18601 - ACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTG - 18660
    -TNVQLAFLLHQILMPAGIIL
    - Q T C N L L F Y F I R Y L C L L E S F C
      KRATCFSTSSDTYACWNHSV
18661 - TGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGTTCAGCAGTGGGGCTTTACGG - 18720
    -WVLTMSITHL * LMFSSGALR
    - G F * L C L * P I Y D * C S A V G L Y G
      G F D Y V Y N P F M I D V Q Q W G F T G
18721 - GTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTA - 18780
    -V T F R V T M T N I A R Y M E M H M W L
     * P S E * P * P T L P G T W K C T C G *
     N L Q S N H D Q H C Q V H G N A H V A S
18781 - GTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTG - 18840
    -V V M L S * L D V * Q S M S A L L S A L
    - L * C Y H D * M F S S P * V L C * A R *
      C D A I M T R C L A V H E C F V K R V D
18841 - ATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAA - 18900
    -I G L L N T L L * E M N * G L I L L A E
    - L V C * I P Y Y R R * T E G * F C L Q K
     W S V E Y P I I G D E L R V N S A C R K
18901 - AAGTACAACACTGGTTGTGAAGTCTGCATTGCTTGATAAGTTTCCAGTTCTTCATG - 18960
    -KYNTWL*SLHCLLISFQFFM
     STTHGCEVCIAC**VSSSS*
      V O H M V V K S A L L A D K F P V L H D
18961 - ACATTGGAAATCCAAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCT - 19020
    -TLEIQRLSSVCLRLK*NGSS
    - H W K S K G Y Q V C A S G * S R M E V L
      I G N P K A I K C V P Q A E V E W K F Y
19021 - ACGATGCTCAGCCATGTAGTGACAAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATG - 19080
    -TMLSHVVTKLTK*RNSSILM
     RCSAM * * QSLQNRGTLLFLC
      D A Q P C S D K A Y K I E E L F Y S Y A
19081 - CTACACATCACGATAAATTCACTGATGGTGTTTGTTTTGGGAATTGTAACGTTGATC - 19140
    -L H I T I N S L M V F V C F G I V T L I
     YTSR*IH*WCLFVLEL*R*S
      T H H D K F T D G V C L F W N C N V D R
19141 - GTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACTTGAACT - 19200
    -V T Q P M Q L C V G L T Q E S C Q T * T
     LPSQCNCV * V * H K S L V K L E L
      Y P A N A I V C R F D T R V L S N L N L
-Y Q A V M V V C M * I S M H S T L Q L
     TRL * W W * F V C E * A C I P H S S F
      P G C D G G S L Y V N K H A F H T P A F
-SIKVHLLI*SNCLSFTILIV
       * K C I Y * F K A I A F L L L F * * S
      D K S A F T N L K Q L P F F Y Y S D S P
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19321 - CTTGTGAGTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTCAAATCTG - 19380
    -LVSLMANK * CRILIMFHSNL
    - L * V S W Q T S S V G Y * L C S T Q I C
       C E S H G K Q V V S D I D Y V P L K S A
19381 - CTACGTGTATTACACGATGCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGT - 19440
     \hbox{--L R V L H D A I * V V L F A D T M Q M S} 
    - Y V Y Y T M Q F R W C C L Q T P C K * V
       T C I T R C N L G G A V C R H H A N E Y
19441 - ACCGACAGTACTTGGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTT - 19500
    -T D S T W M H I I * * F L L D L A Y G F
    - P T V L G C I * Y D D F C W I * P M D L
      R Q Y L D A Y N M M I S A G F S L W I Y
19501 - ACAAACAATTTGATACTTATAACCTGTGGAATACATTTACCAGGTTACAGAGTTTAGAAA - 19560
    -TNNLILITCGIHLPGYRV*K
    - Q T I * Y L * P V E Y I Y Q V T E F R K
       K Q F D T Y N L W N T F T R L Q S L E N
19561 - ATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCGAAGCACCTG - 19620
    -M W L I M L L I K D T L M D T P A K H L
    - C G L * C C * * R T L * W T R R R S T C
      V A Y N V V N K G H F D G H A G E A P V
19621 - TTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTG - 19680
    -FPSLIMLFTQR*MVLMWRSL
    - F H H * * C C L H K G R W Y * C G D L *
      S I I N N A V Y T K V D G I D V E I F E
19681 - AAAATAAGACACACTTCCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTA - 19740
    -KIRQHFLLMLHLSFGLSVTL
    - K * D N T S C * C C I * A L G * A * H *
      N K T T L P V N V A F E L W A K R N I K
19741 - AACCAGTGCCAGAGATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTG - 19800
    -N Q C Q R L R Y S I I W V L I S L L I L
    - T S A R D * D T Q * F G C * Y R C * Y C
      P V P E I K I L N N L G V D I A A N T V
19801 - TAATCTGGGACTACAAAAGAGAAGCCCCAGCACATGTATCTACAATAGGTGTCTGCACAA - 19860
    - * S G T T K E K P Q H M Y L Q * V S A Q
    - N L G L Q K R S P S T C I Y N R C L H N
      I W D Y K R E A P A H V S T I G V C T M
19861 - TGACTGACATTGCCAAGAAACCTACTGAGAGTGCTTGTTCTCACTTACTGTCTTGTTTG - 19920
    - * L T L P R N L L R V L V L H L L S C L
    - D * H C Q E T Y * E C L F F T Y C L V *
      T D I A K K P T E S A C S S L T V L F D
19921 - ATGGTAGAGTGGAAGGACAGGTAGACCTTTTTAGAAACGCCCGTAATGGTGTTTTAATAA - 19980
    -MVEWKDR*TFLETPVMVF**
    - W * S G R T G R P F * K R P * W C F N N
      G R V E G O V D L F R N A R N G V L I T
19981 - CAGAAGGTTCAGTCAAAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCAATG - 20040
    -QKVQSKV * HLQRDQHKLASM
    - R R F S Q R S N T F K G T S T S * R Q W
       E G S V K G L T P S K G P A Q A S V N G
20041 - GAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACG - 20100
    -ESH*LENQ*KHSLTTLRK*T
    - S H I N W R I S K N T V * L L * E S R R
      V T L I G E S V K T Q F N Y F K K V D G
20101 - GCATTATTCAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTA - 20160
    -ALFNSCLKPTLLRAET*RIL
    - H Y S T V A * N L L Y S E Q R L R G F *
       I I Q Q L P E T Y F T Q S R D L E D F K
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20161 - AGCCCAGATCACAAATGGAAACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGC - 20220
    -SPDHKWKLTFSSSLWMNSYS
    - A Q I T N G N * L S R A R Y G * I H T A
      PRSQMETDFLELAMDEFIQR
20221 - GATATAGCTCGAGGGCTATGCCTTCGAACACATCGTTTATGGAGATTTCAGTCATGGAC - 20280
    -DISSRAMPSNTSFMEISVMD
    - I * A R G L C L R T H R L W R F Q S W T
      YKLEGYAFEHIVYGDFSHGQ
20281 - AACTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGCTCACAAGATTCACCACTTA - 20340
    -N L A V F I * * * A * P S A H K I H H L
    - T W R S S F N D R L S Q A L T R F T T *
      LGGLHLMIGLAKRSQDSPLK
20341 - AATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGC - 20400
    -N * R I L S L W T A Q * K I T S * Q M R
    - I R G F Y P Y G Q H S E K L L H N R C A
      L E D F I P M D S T V K N Y F I T D A Q
20401 - AAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTCG - 20460
    -KOVHONVCVL*LIFYLMTLS
    - N R F I K M C V F C D * S F T * * L C R
      T G S S K C V C S V I D L L L D D F V E
20461 - AGATAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACT - 20520
    -R * * S H K I C Q * F Q K W S R L Q L T
    - D N K V T R F V S D F K S G Q G Y N * L
      I I K S Q D L S V I S K V V K V T I D Y
20521 - ATGCTGAAATTTCATTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAA - 20580
    -MLKFHSCFGVRMDMLKPSTQ
    - C * N F I H A L V * G W T C * N L L P K
     A E I S F M L W C K D G H V E T F Y P K
20581 - AACTACAAGCAAGTCAAGCGTGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGC - 20640
    -NYKOVKRGNOVLRCLTCTRC
    - T T S K S S V A T R C C D A * L V Q D A
     L Q A S Q A W Q P G V A M P N L Y K M Q
20641 - AAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAA - 20700
    -KECFLKSVTFRIMVKMLLYQ
    - K N A S * K V * P S E L W * K C C Y T K
      R M L L E K C D L Q N Y G E N A V I P K
20701 - AAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATACTTAAATACACTTA - 20760
    -KE * * * M S Q S I L N C V N T * I H L
     RNNDECRKVYSTVSILKYTY
      G I M M N V A K Y T Q L C Q Y L N T L T
20761 - CTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGGTGCTGGCTCTGATAAAGGAG - 20820
    -L * L Y P T T * E L F T L V L A L I K E
    - F S C T L Q H E S Y S L W C W L * * R S
     LAVPYNMRVIHFGAGSDKGV
20821 - TTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTCGATT - 20880
    -L H Q V Q L C S D N G C Q L A H Y L S I
     CTRYSCAQTMVANWHTTCRF
     A P G T A V L R Q W L P T G T L L V D S
20881 - CAGATCTTAATGACTTCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAG - 20940
    -QILMTSSPTQILL * LETVQQ
    - R S * * L R L R R F Y F N W R L C N S
     D L N D F V S D A D S T L I G D C A T V
-YIRLINGTLLLAICMTLGPN
     T Y G * * M G P Y Y * R Y V * P * D Q T
      H T A N K W D L I I S D M Y D P R T K H
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21001 - ATGTGACAAAAGAGAATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGTGGATTTATAA - 21060
    -M * Q K R M T L K K G F S L I C V D L *
    - C D K R E * L * R R V F H L S V W I Y K
- V T K E N D S K E G F F T Y L C G F I K
21061 - AGCAAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAACAGAGCATTCTTGGAATG - 21120
    - S K N * P W V V L * L * R * Q S I L G M
    - A K T S P G W F Y S C K D N R A F L E C
      Q K L A L G G S I A V K I T E H S W N A
21121 - CTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTACAAATGTAA - 21180
    -LTFTSLWAISHGGQLLLQM*
    - * P L Q A Y G P F L M V D S F C Y K C K
      D L Y K L M G H F S W W T A F V T N V N
21181 - ATGCATCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAAC - 21240
    -MHHHRKHF*LGLTILASRRN
    - C I I I G S I F N W G * L S W Q A E G T
      ASSSEAFLIGANYLGKPKEQ
21241 - AAATTGATGGCTATACCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCC - 21300
    -KLMAIPCMLTTFSGGTQILS
    - N * W L Y H A C * L H F L E E H K S Y P
      I D G Y T M H A N Y I F W R N T N P I Q
21301 - AGTTGTCTTCCTATTCACTCTTTGACATGAGCAAATTTCCTCTTAAATTAAGAGGAACTG - 21360
    -SCLPIHSLT * ANFLLN * EEL
    - V V F L F T L * H E Q I S S * I K R N C
      LSSYSLFDMSKFPLKLRGTA
21361 - CTGTAATGTCTCTTAAGGAGAATCAAATCAATGATATGATTTATTCTCTTCTGGAAAAAG - 21420
    -L * C L L R R I K S M I * F I L F W K K
    - C N V S * G E S N Q * Y D L F S S G K R
      V M S L K E N Q I N D M I Y S L L E K G
21421 - GTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGTTTCAAGTGATATTCTTGTTAACA - 21480
    -VGLSLEKTTELWFQVIFLLT
    - * A Y H * R K Q Q S C G F K * Y S C * Q
      R L I I R E N N R V V V S S D I L V N N
21481 - ACTAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTG - 21540
    -T K R T C L F S Y Y F L L S L V V V T L
    - L N E H V Y F L I I S Y S H * W * * P *
      * T N M F I F L L F L T L T S G S D L D
21541 - ACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTA - 21600
    -TGAPLLMMFKLLITLNILHL
    - P V H H F * * C S S S * L H S T Y F I Y
      R C T T F D D V Q A P N Y T Q H T S S M
- * G G F T I L M K F L D Q T L F I * L R
    - E G G L L S * * N F * I R H S L F N S G
      R G V Y Y P D E I F R S D T L Y L T Q D
21661 - ATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTG - 21720
    -IYFFHFILMLQGFILLIIRL
    - FISSILF * CYRVSYY * SYVW
      LFLPFYSNVTGFHTINHTFG
21721 - GCAACCCTGTCATACCTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATG - 21780
    -ATLSYLLRMVFILLPQRNQM
    - O P C H T F * G W Y L F C C H R E I K C
      N P V I P F K D G I Y F A A T E K S N V
21781 - TTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTA - 21840
    -LSVVGFLVLP*TTSHSR*LL
    - C P W L G F W F Y H E Q Q V T V G D Y Y
       V R G W V F G S T M N N K S Q S V I I I
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21841 - TTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGAATTGTGTGACAACCCTT - 21900
    -LTILLMLLYEHVTLNCVTTL
      * Q F Y * C C Y T S M * L * I V * Q P F
       N N S T N V V I R A C N F E L C D N P F
21901 - TCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATAATGCAT - 21960
    -SLLFLNPWVHRHIL*YSIMH
    - L C C F * T H G Y T D T Y Y D I R * C I
      F A V S K P M G T Q T H T M I F D N A F
21961 - TTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAG - 22020
    -LIALSSTYLMPFRLMFQKSQ
      * L H F R V H I * C L F A * C F R K V R
       N C T F E Y I S D A F S L D V S E K S G
22021 - GTAATTTTAAACACTTACGAGAGTTTGTGTTTTAAAAATAAAGATGGGTTTCTCTATGTTT - 22080
    -VILNTYESLCLKIKMGFSMF
    - * F * T L T R V C V * K * R W V S L C L
       N F K H L R E F V F K N K D G F L Y V Y
22081 - ATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGA - 22140
    -IRAINL * M * F V I Y L L V L T L *
    - * G L S T Y R C S S * S T F W F * H F E
      K G Y Q P I D V V R D L P S G F N T L K
22141 - AACCTATTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAG - 22200
    -NLFLSCLLVLTLQILEPFLQ
    - T Y F * V A S W Y * H Y K F * S H S Y S
      PIFKLPLGINITNFRAILTA
22201 - CCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTTGGCTATT - 22260
    -PFHLLKTFGARQLQPILLAI
    - L F T C S R H L G H V S C S L F C W L F
      F S P A Q D I W G T S A A A Y F V G Y L
22261 - TAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTG - 22320
    - * S O L H L C S S M M K M V Q S Q M L L
    - K A N Y I Y A O V * * K W Y N H R C C *
       K P T T F M L K Y D E N G T I T D A V D
22321 - ATTGTTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA - 22380
    -IVLKIHLLNSNALLRALRLT
    - L F S K S T C * T Q M L C * E L * D * Q
       C S Q N P L A E L K C S V K S F E I D K
22381 - AAGGAATTTACCAGACCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCC - 22440
    - K E F T R P L I S G L F P Q E M L * D S - R N L P D L * F Q G C S L R R C C E I P
       G I Y Q T S N F R V V P S G D V V R F P
22441 - CTAATATTACAAACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTG - 22500
    -LILQTCVLLERFLMLLNSLL
      * Y Y K L V S F W R G F * C Y * I P F C
       N I T N L C P F G E V F N A T K F P S V
22501 - TCTATGCATGGGAGAAAAAAATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACA - 22560
    - S M H G R E K K F L I V L L I T L C S T - L C M G E K K N F * L C C * L L C A L Q
       Y A W E R K K I S N C V A D Y S V L Y N
22561 - ACTCAACATTTTTTCAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGTTGAATGATC - 22620
    -TQHFFQPLSAMAFLPLS*MI
    - L N I F F N L * V L W R F C H * V E * S
       S T F F S T F K C Y G V S A T K L N D L
22621 - TTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAA - 22680
    -FASPMSMQILL*SREMM*DK
     LLLQCLCRFFCSQGR*CKTN
       C F S N V Y A D S F V V K G D D V R Q I
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22681 ~ TAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAATTGCCAGATGATTTCA - 22740
    - * R Q D K L V L L I I I I N C Q M I S
    - S A R T N W C Y C * L * L * I A R * F H
       A P G Q T G V I A D Y N Y K L P D D F M
22741 - TGGGTTGTCCTTGCAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATA - 22800
    -W V V S L L G I L G T L M L L Q L V I I
    - G L C P C L E Y * E H · * C Y F N W * L *
       G C V L A W N T R N I D A T S T G N Y N
-IINIGILDMASLGPLRETYL
    - L * I * V S * T W Q A * A L * E R H I *
       Y K Y R Y L R H G K L R P F E R D I S N
22861 - ATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGC - 22920
    -MCLSPLMANLAPHLLLIVIG
    - C A F L P * W Q T L H P T C S * L L L A
       V P F S P D G K P C T P P A L N C Y W P
22921 - CATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTG - 22980
    -H * M I M V F T P L L A L A T N L T E L
    - I K * L W F L H H Y W H W L P T L Q S C
    - L N D Y G F Y T T G I G Y Q P Y R V V
22981 - TAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCA - 23040
    - * Y F L L N F * M H R P R F V D Q N Y P
    - S T F F * T F K C T G H G L W T K I I H
       V L S F E L L N A P A T V C G P K L S T
23041 - CTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTG - 23100
    - L T L L R T S V S I L I L M D S L V L V
- * P Y * E P V C Q F * F * W T H W Y W C
       D L I K N Q C V N F N F N G L T G T G V
23101 - TGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTG - 23160
    -C * L L Q R D F N H F N N L A V M F L
    - V N S F F K E I S T I S T I W P * C F *
    - LTPSSKRFQPFQQFGRDVSD
23161 - ATTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCT - 23220
    -ISLIPFEILKHLKY*TFHLA
    - F H * F R S R S * N I * N I R H F T L L
      F T D S V R D P K T S E I L D I S P C S
23221 - CTTTTGGGGGTGTAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTC - 23280
    - L L G V * V * L H L E Q M L H L K L L F
- F W G C K C N Y T W N K C F I * S C C S
      F G G V S V I T P G T N A S S E V A V L
23281 - TATATCAAGATGTTAACTGCACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACAC - 23340
    -YIKMLTALMFLQQFMQINSH
     ISRC*LH*CFYSNSCRSTHT
       Y Q D V N C T D V S T A I H A D Q L T P
23341 - CAGCTTGGCGCATATATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTA - 23400
     -QLGAYILLETMYSRLKQAVL
       SLAHIFYWKQCIPDSSRLSY
       AWRIYSTGNNVFQTQAGCLI
23401 - TAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAGCTGGCATTT - 23460
    - * E L S M S T L L M S A T F L L E L A F
- R S * A C R H F L * V R H S Y W S W H L
- G A E H V D T S Y E C D I P I G A G I C
23461 - GTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTT - 23520
    - V L V T I Q F L Y Y V V L A K N L L W L - C * L P Y S F F I T * Y * P K I Y C G L
       A S Y H T V S L L R S T S Q K S I V A Y
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23521 - ATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATAC - 23580
    -I L C L * V L I V Q L L T L I T P L L Y
      YYVFRC**FNCLL**HHCYT
        T M S L G A D S S I A Y S N N T I A I P
23581 - CTACTAACTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCT - 23640
    -LLTFQLALLQK*CLFLWLKP
    - Y * L F N * H Y Y R S N A C F Y G * N L
        TNFSISITTEVMPVSMAKTS
23641 - CCGTAGATTGTAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCC - 23700
    - P * I V I C T S A E I L L N V L I C F S - R R L * Y V H L R R F Y * M C * F A S P
       V D C N M Y I C G D S T E C A N L L L Q
23701 - AATATGGTAGCTTTTGCACACAACTAAATCGTGCACTCTCAGGTATTGCTGCTGAACAGG - 23760
    -N M V A F A H N * I V H S Q V L L L N R
    - I W * L L H T T K S C T L R Y C C * T G
        Y G S F C T Q L N R A L S G I A A E Q D
23761 - ATCGCAACACGTGAAGTGTTCGCTCAAGTCAAACAAATGTACAAAACCCCAACTTTGA - 23820
    -I A T H V K C S L K S N K C T K P Q L *
    - S Q H T * S V R S S Q T N V Q N P N F E
        RNTREVFAQVKQMYKTPTLK
23821 - AATATTTTGGTGGTTTTTAATTTTTCACAAATATTACCTGACCCTCTAAAGCCAACTAAGA - 23880
    -NILVVLIFHKYYLTL * SQLR
      IFWWF*FFTNIT*PSKAN*E
       Y F G G F N F S Q I L P D P L K P T K R
23881 - GGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGA - 23940
    -G L L L R T C S L I R * H S L M L A S * - V F Y * G L A L * * G D T R * C W L H E
        S F I E D L L F N K V T L A D A G F M K
23941 - AGCAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGT - 24000
    - S N M A N A * V I L M L E I S F V R R S - A I W R M P R * Y * C * R S H L C A E V
        O Y G E C L G D I N A R D L I C A Q K F
24001 - TCAATGGACTTACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTG - 24060
     -SMDLQCCHLCSLMI*LLPTL
    - Q W T Y S V A T S A H * * Y D C C L H C
       NGLTVLPPLLTDDMIAAYTA
24061 - CTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTC - 24120
    - L L * L V V L P L L D G H L V L A L L F - C S S * W Y C H C W M D I W C W R C S S
      ALVSGTATAGWTFGAGAALQ
24121 - AAATACCTTTTGCTATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATG - 24180
     -KYLLLCKWHIGSMALELPKM
    - N T F C Y A N G I * V Q W H W S Y P K C
       I P F A M Q M A Y R F N G I G V T Q N V
24181 - TTCTCTATGAGAACCAAAACCAATTGCCCAACCAATTTAACAAGGCGATTAGTCAAATTC - 24240
     -FSMRTKNKSPTNLTRRLVKF
-SL*EPKTNRQPI*QGD*SNS
       LYENQKQIANQFNKAISQIQ
24241 - AAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGA - 24300
     -KNHLQQHQLHWASCKTLLTR
      RITYNNINCIGQAARRC*PE
         \hbox{\tt E} \hbox{\tt S} \hbox{\tt L} \hbox{\tt T} \hbox{\tt T} \hbox{\tt T} \hbox{\tt S} \hbox{\tt T} \hbox{\tt A} \hbox{\tt L} \hbox{\tt G} \hbox{\tt K} \hbox{\tt L} \hbox{\tt Q} \hbox{\tt D} \hbox{\tt V} \hbox{\tt V} \hbox{\tt N} \hbox{\tt Q} \hbox{\tt N} \\
24301 - ATGCTCAAGCATTAAACACCTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAA - 24360
     -MLKH*THLLNNLALILVQFQ
      CSSIKHTC*TT*L*FWCNFK
        A Q A L N T L V K Q L S S N F G A I S S
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24361 - GTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACA - 24420
    -VC * M I S F R D L I K S R R Y K L T
    - C A K * Y P F A T * * S R G G T N * Q
      V L N D I L S R L D K V E A E V Q I D R
24421 - GGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGG - 24480
    -G * L Q A D F K A F K P M * H N N * S G
    - V N Y R Q T S K P S N L C N T T T N Q G
       LITGRLQSLQTYVTQQLIRA
24481 - CTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTAAAATGTCTGAGTGTGTTCTTG - 24540
    -LLKSGLLLILLLKCLSVFL
    - C * N Q G F C * S C C Y * N V * V C S W
       A E I R A S A N L A A T K M S E C V L G
24541 - GACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAG - 24600
    -DNQKELTFVERATTLCPSHK
    - T I K K S * L L W K G L P P Y V L P T S
       Q S K R V D F C G K G Y H L M S F P Q A
24601 - CAGCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGAGAGGAACT - 24660
    - Q P R M V L S S Y M S R M C H P R R G T
    - S P A W C C L P T C H V C A I P G E E L
       A P H G V V F L H V T Y V P S Q E R N F
24661 - TCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTT - 24720
    -SPQRQQFVMKAKHTSLVKVF
    - H H S A S N L S * R Q S I L P S * R C F
       T T A P A I C H E G K A Y F P R E G V F
24721 - TTGTGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAA - 24780
    -LCLMALLGLLHRGTSFLHK*
      C V * W H F L V Y Y T E E L L F S T N N
      V F N G T S W F I T Q R N F F S P Q I I
24781 - TTACTACAGACAATACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACA - 24840
    -LLQTIHLSQEIVMSLLASLT
     YYRQYICLRKL*CRYWHH*Q
       TTDNTFVSGNCDVVIGIINN
24841 - ACACAGTTTATGATCCTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGT - 24900
    -TQFMILCNLSLTHSKKSWTS
    - H S L * S S A T * A * L I Q R R A G Q V
      TVYDPLQPELDSFKEELDKY
24901 - ACTTCAAAAATCATACATCACCAGATGTTGATCTTGGCGACATTTCAGGCCATTAACGCTT - 24960
    -TSKIIHHQMLILATFQALTL
-LQKSYITRC*SWRHFRH*RF
       F K N H T S P D V D L G D I S G I N A S
24961 - CTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATG - 25020
    - L S S T F K K K L T A S M R S L K I * M
- C R Q H S K R N * P P Q * G R * K F K *
       V V N I Q K E I D R L N E V A K N L N E
25021 - AATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTGGT - 25080
    -NHSLTFKNWENMSNILNGLG
      ITH*PSRIGKI*AIY*MALV
       SLIDLQELGKYEQYIKWPWY
25081 - ATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTT - 25140
    -MFGSASLLD*LPSSWLQSCF
-CLARLHCWTNCHRHGYNLAL
       V W L G F I A G L I A I V M V T I L L C
25141 - GTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCA - 25200
    - V A * L V V A V A S R V H A L V V L A A
- L H D * L L Q L P Q G C M L L W F L L Q
       C M T S C C S C L K G A C S C G S C C K
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25201 - AGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAA - 25260
    -SLMRMTLSQFSRVSNYITHK
    - V * * G * L * A S S Q G C Q I T L H I N
       FDEDDSEPVLKGVKLHYT*T
25261 - CGAACTTATGGATTTGTTTATGAGATTTTTTACTCTTGGATCAATTACTGCACAGCCAGT - 25320
    -RTYGFVYEIFYSWINYCTAS
    - ELM DLF M R F F T L G S I T A Q P V
       NLWICL * DFLLLDQLLHSQ *
25321 - AAAAATTGACAATGCTTCTCCTGCAAGTACTGTTCATGCTACAGCAACGATACCGCTACA - 25380
    - K N * Q C F S C K Y C S C Y S N D T A T
    - K I D N A S P A S T V H A T A T I P L Q
      K L T M L L L Q V L F M L Q Q R Y R Y K
25381 - AGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTCAGAG - 25440
    -S L T P F R M A C Y W R C I S C C F S E
    - A S L P F G W L V I G V A F L A V F Q S
       P H S L S D G L L L A L H F L L F F R A
25441 - CGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCA - 25500
    -RYQNNCAQ*KMAASPL*GLP
    - A T K I I A L N K R W Q L A L Y K G F Q
      L P K * L R S I K D G S * P F I R A S S
25501 - GTTCATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTCGC - 25560
    -V H L Q F T A A I C Y H L F T S F A C R
    - FICNLLLEVTIYSHLLLVA
       S F A I Y C C Y L L P S I H I F C L S L
25561 - TGCAGGTAAGGAGGCGCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCAT - 25620
    -CR*GGAIFVPLCLDIFSTMH
    - A G K E A Q F L Y L Y A L I Y F L Q C I
- Q V R R R N F C T S M P * Y I F Y N A S
25621 - CAACGCATGTAGAATTATTATGAGATGTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCC - 25680
    -QRM*NYYEMLALLEVQIQEP
    - N A C R I I M R C W L C W K C K S K N P
       T H V E L L * D V G F V G S A N P R T H
-I T L * C Q L L C L L A H T * L * L L Y
     L L Y D A N Y F V C W H T H N Y D Y C I
      Y F M M P T T L F A G T H I T M T T V Y
25741 - ACCATATAACAGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGGCATTTCAACACC - 25800
    -T I * Q C H R Y N C R Y * R * R H F N T
     P Y N S V T D T I V V T E G D G I S T P
       HITVSQIQLSLLKVTAFQHQ
25801 - AAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTAA - 25860
    -KTQRRLPNWWLF*G*ALRC*
     K L K E D Y Q I G G Y S E D R H S G V K
      N S K K T T K L V V I L R I G T Q V L K
25861 - AGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTACTACCAGCTTGAGTCTACACA - 25920
    -RLCRCTWLFHRSLLPA * V Y T
     D Y V V H G Y F T E V Y Y Q L E S T Q
       T M S L Y M A I S P K F T T S L S L H K
25921 - AATTACTACAGACACTGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAA - 25980
    -N Y Y R H W Y * K C Y I L H L * Q A C *
     I T T D T G I E N A T F F I F N K L V K
      L L Q T L V L K M L H S S S L T S L L K
25981 - AGACCCACCGAATGTGCAAATACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGC - 26040
    -RPTECANTHNRRLFRSC*SS
    - D P P N V Q I H T I D G S S G V A N P A
       T H R M C K Y T Q S T A L Q E L L I Q Q
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26041 - AATGGATCCAATTTATGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAGA - 26100
     -NGSNL**ADDDY*RAFVSTR
       M D P I Y D E P T T T T S V P L * A Q E
        WIQFMMSRRRLLACLCKHKK
26101 - AAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACAGGTACGTTAATAGTTAA - 26160
     - K * V R T Y V L I R F G R N R Y V N S *
       S E Y E L M Y S F V S E E T G T L I V N
         \begin{smallmatrix} V \end{smallmatrix} S \begin{smallmatrix} T \end{smallmatrix} N \begin{smallmatrix} L \end{smallmatrix} C \begin{smallmatrix} T \end{smallmatrix} H \begin{smallmatrix} S \end{smallmatrix} F \begin{smallmatrix} R \end{smallmatrix} K \begin{smallmatrix} K \end{smallmatrix} Q \begin{smallmatrix} V \end{smallmatrix} R * * L \begin{smallmatrix} I \end{smallmatrix}
26161 - TAGCGTACTTCTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCATCCTTAC - 26220
          \hbox{\tt R} \ \hbox{\tt T} \ \hbox{\tt S} \ \hbox{\tt F} \ \hbox{\tt S} \ \hbox{\tt C} \ \hbox{\tt F} \ \hbox{\tt R} \ \hbox{\tt G} \ \hbox{\tt I} \ \hbox{\tt L} \ \hbox{\tt A} \ \hbox{\tt S} \ \hbox{\tt H} \ \hbox{\tt T} \ \hbox{\tt S} \ \hbox{\tt H} \ \hbox{\tt P} \ \hbox{\tt Y} 
       S V L L F L A F V V F L L V T L A I L T
        AYFFFLLSWYSC*SH*PSLL
26221 - TGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAAC - 26280
     -CASIVCVLLQYC*REFSKTN
       A L R L C A Y C C N I V N V S L V K P T
        R F D C V R T A A I L L T * V * * N Q R
26281 - GGTTTACGTCTACTCGCGTGTTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCT - 26340
     -GLRLLAC * KSELF * RSS * SS
     - V Y V Y S R V K N L N S S E G V P D L L
        FTSTRVLKI*TLLKEFLIFW
26341 - GGTCTAAACGAACTAACTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATG - 26400
     -G L N E L T I I I L F G T L T L L I M
       S K R T N Y Y Y Y S V W N F N I A Y H G
26401 - GCAGACAACGGTACTATTACCGTTGAGGAGCTTAAACAACTCCTGGAACAATGGAACCTA - 26460
     - A D N G T I T V E E L K Q L L E Q W N L
       Q T T V L L P L R S L N N S W N N G T *
        R Q R Y Y Y R * G A * T T P G T M E P S
26461 - GTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACTACAATTTGCCTATTCTAATCGG - 26520
     -VIGFLFLAWIMLLQFAYSNR
-**VSYS*PGLCYYNLPILIG
        N R F P I P S L D Y V T T I C L F * S E
26521 - AACAGGTTTTTGTACATAATAAAGCTTGTTTTCCTCTGGCTCTTGTGGCCAGTAACACTT - 26580
     -NRFLYIIKLVFLWLLWPVTL
      TGFCT**SLFSSGSCGQ*HL
        Q V F V H N K A C F P L A L V A S N T C
26581 - GCTTGTTTTGTGCTTGCTGTTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT - 26640
     -ACFVLAVVYRINWVTGGIAI
      L V L C L L S T E L I G * L A G L R L L F C A C C C L Q N * L G D W R D C D C
-A M A C I V G L M W L S Y F V A S F R L
      Q W L V L * A * C G L A T S L L P S G C N G L Y C R L D V A * L L R C F L Q A V
-FARTRSMWSFNPETNILLNV
      L L V P A Q C G H S T Q K Q T F F S M C
        C S Y P L N V V I Q P R N K H S S Q C A
26761 - CCTCTCCGGGGGACAATTGTGACCAGACCGCTCATGGAAAGTGAACTTGTCATTGGTGCT - 26820
     - P L R G T I V T R P L M E S E L V I G A
- L S G G Q L * P D R S W K V N L S L V L
        S P G D N C D Q T A H G K * T C H W C C
26821 - GTGATCATTCGTGGTCACTTGCGAATGGCCGGACACTCCCTAGGGCGCTGTGACATTAAG - 26880
     -VIIRGHLRMAGHSLGRCDIK
         S F V V T C E W P D T P * G A V T L R
        D H S W S L A N G R T L P R A L * H * G
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26881 - GACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGA - 26940
    -D L P K E I T V A T S R T L S Y Y K L G
     TCQKRSLWLHHERFLITN*E
      P A K R D H C G Y I T N A F L L Q I R S
26941 - GCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTATTGGA - 27000
    - A S Q R V G T D S G F A A Y N R Y R I G
     RRSV * ALIQVLLH T T A T V L E
      V A A C R H * F R F C C I Q P L P Y W K
27001 - AACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAG - 27060
    -NYKLNTDHAGSNDNIALLVQ
      TIN * I Q T T P V A T T I L L C * Y S
      L * I K Y R P R R * Q R Q Y C F A S T V
27061 - TAAGTGACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGAT - 27120
    - * V T T D V S S C * L P G Y N S R D I D
    - K * Q Q M F H L V D F Q V T I A E I L I
      S D N R C F I L L T S R L Q * Q R Y * L
27121 - TATCATTATGAGGACTTTCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAAT - 27180
    -YHYEDFQDCYLES*RYNKFN
      IIMRTFRIAIWNLDVIISSI
      SL*GLSGLLFGILTL**VQ*
27181 - AGTGAGACAATTATTTAAGCCTCTAACTAAGAAGAATTATTCGGAGTTAGATGATGAAGA - 27240
    -SETII * A S N * E E L F G V R * * R
      V R Q L F K P L T K K N Y S E L D D E E
      * D N Y L S L * L R R I I R S * M M K N
27241 - ACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAATTATTCTCTTCCTGACATTGA - 27300
    -TYGVRLSIKRT * KLFSS * H *
     PMELDYP*NEHENYSLPDID
      L W S * I I H K T N M K I I L F L T L I
27301 - TTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGTACGACTGTAC - 27360
    -LYLHLASYITIRSVLEVRLY
    - CIYILRAISLSGVC * RYDC T
      V F T S C E L Y H Y Q E C V R G T T V L
27361 - TACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAATTCACCATTTCACCCTCTTG - 27420
    -y * K N L A H Q E H T R A I H H F T L L
     T K R T L P I R N I R G Q F T I S P S C
      LKEPCPSGTYEGNSPFHPLA
27421 - CTGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGTGCTGACG - 27480
    -L T I N L H * L A L A H T L L L V L T
       Q * I C T N L H * H T L C F C L C * R
      D N K F A L T C T S T H F A F A C A D G
27481 - GTACTCGACATACCTATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGAC - 27540
    -V L D I P I S C V Q D Q F H Q N F S S D
     Y S T Y L S A A C K I S F T K T F H Q T
      TRHTYQLRARS V S P K L F I R Q
27541 - AAGAGGAGGTTCAACAAGAGCTCTACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTAT - 27600
    -KRRFNKSSTRHFFSLLLL*Y
    - R G G S T R A L L A T F S H C C C S S I
      E E V Q Q E L Y S P L F L I V A A L V F
-F * Y F A S P L R E R Q N E * A H F N *
     FNTLLHH*EKDRMNELTLID
      LILCFTIKRKTE * M S S L * L T
27661 - CTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTTTTAATAATGCTTATTATATT - 27720
    -LLFVLFSLSAIPCFNNAYYI
      FYLCFLAFLVLIMLIIF
      SICAF * PFCYSLF * * CLLYF
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27721 - TTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGAACAT - 27780
    -LVFTRNPGSRRTLYQSLNEH
    - W F S L E I Q D L E E P C T K V * T N M
      G F H S K S R I * K N L V P K S K R T *
27781 - GAAACTTCTCATTGTTTTGACTTGTATTCTCTATGCAGTTGCATATGCACTGTAGTACA - 27840
    -ETSHCFDLYFSMQLHMHCST
    - K L L I V L T C I S L C S C I C T V V Q
      N F S L F * L V F L Y A V A Y A L * Y S
27841 - GCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGG - 27900
    - A L C I * * T S C A * R S L * G T T L G
    - R C A S N K P H V L E D P C K V Q H * G
      AVHLINLMCLKILVRYNTRG
27901 - GTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGAT - 27960
    -VILIALLGFVL*ERFYLFID
     * Y L * H C L A L C S R K G F T F S * M
      N T Y S T A W L C A L G K V L P F H R W
27961 - GGCACACTATGGTTCAAACATGCACACCTAATGTTACTATCAACTGTCAAGATCCAGCTG - 28020
    -GTLWFKHAHLMLLSTVKIQL
    - A H Y G S N M H T * C Y Y Q L S´R S S W
      H T M V Q T C T P N V T I N C Q D P A G
28021 - GTGGTGCGCTTATAGCTAGGTGTTGGTACCTTCATGAAGGTCACCAAACTGCTGCATTTA - 28080
    - V V R L * L G V G T F M K V T K L L H L
    - W C A Y S * V L V P S * R S P N C C I *
      G A L I A R C W Y L H E G H Q T A A F R
28081 - GAGACGTACTTGTTGTTTTAAATAAACGAACAAATTAAAATGTCTGATAATGGACCCCAA - 28140
    -ETYLLF*INEQIKMSDNGPQ
     RRTCCFK*TNKLKCLIMDPN
      D V L V V L N K R T N * N V * * W T P I
28141 - TCAAACCAACGTAGTGCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAAT - 28200
    -SNORSAPRITFGGPTDSTDN
     O T N V V P P A L H L V D P Q I Q L T I
      KPT * CPPHYIWWTHRFN * Q *
28201 - AACCAGAATGGAGGACGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCC - 28260
    -N Q N G G R N G A R P K Q R R P Q G L P
      T R M E D A M G Q G Q N S A D P K V Y P
      PEWRTQWGKAKTAPTPRFTQ
28261 - AATAATACTGCGTCTTGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTC - 28320
    -NNTASWFTALTQHGKEELRF
     I I L R L G S Q L S L S M A R R N L D S
      * Y C V L V H S S H S A W Q G G T * I P
28321 - CCTCGAGGCCAGGGCGTTCCAATCAACACCAATAGTGGTCCAGATGACCAAATTGGCTAC - 28380
    -PRGQGVPINTNSGPDDQIGY
     L E A R A F Q S T P I V V Q M T K L A T
      SRPGRSNQHQ*WSR*PNWLL
28381 - TACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCC - 28440
    - Y R R A T R R V R G G D G K M K E L S P
     TEELPDEFVVVTAK*KSSAP
      PKSYPTSSWW*RQNERAQPQ
28441 - AGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTCCCTACGGCGCTAAC - 28500
    -R W Y F Y Y L G T G P E A S L P Y G A N
      D G T S I T * E L A Q K L H F P T A L T
      M V L L L P R N W P R S F T S L R R * Q
28501 - AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATT - 28560
    -KEGIVWVATEGALNTPKDHI
     KKASYGLQLREP*IHPKTTL
      R R H R M G C N * G S L E Y T Q R P H W
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28561 - GGCACCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACA - 28620
    -G T R N P N N N A A T V L Q L P Q G T T
    - A P A I L I T M L P P C Y N F L K E Q H
       HPQS**QCCHRATTSSRNNI
28621 - TTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCC - 28680
    -LPKGFYAEGSRGGSQASSRS
    - C Q K A S T Q R E A E A A V K P L L A P
       A K R L L R R G K Q R R Q S S L F S L L
28681 - TCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT - 28740
    -SSRSRGNSRNSTPGSSRGNS
    - H H V V A V I Q E I Q L L A A V G E I L
       I T * S R * F K K F N S W Q Q * G K F S
28741 - CCTGCTCGAATGCCTAGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGACAGA - 28800
    -PARMASGGETALALLLDR
    - L L E W L A E V V K L P S R Y C C * T D
       C S N G * R R W * N C P R A I A A R Q I
28801 - TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTC - 28860
    -L N Q L E S K V S G K G Q Q Q G Q T V
      * T S L R A K F L V K A N N N K A K L S
       EPA*EQSFW*RPTTTRPNCH
28861 - ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAA - 28920
    -T K K S A A E A S K K P R Q K R T A T K
     LRNLLRHLKSLAKNVLPQN
       * E I C C * G I * K A S P K T Y C H K T
28921 - CAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAACCCAAGGAAATTTC - 28980
    -QYNVTQAFGRRGPEQTQGNF
    - S T T S L K H L G D V V Q N K P K E I S
       V O R H S S I W E T W S R T N P R K F R
28981 - GGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAA - 29040
    -G D Q D L I R Q G T D Y K H W P Q I A Q
    - G T K T * S D K E L I T N I G R K L H N
       G P R P N Q T R N * L Q T L A A N C T I
29041 - TTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT - 29100
    -FAPSASAFFGMSRIGMEVTP
    - L L Q V P L H S L E C H A L A W K S H L
       C S K C L C I L W N V T H W H G S H T F
29101 - TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTC - 29160
    - S G T W L T Y H G A I K L D D K D P Q F - R E H G * L I M E P L N W M T K I H N S - G N M A D L S W S H * I G * Q R S T I Q
29161 - AAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACA - 29220
    -K D N V I L L N K H I D A Y K T F P P T
    - K T T S Y C * T S T L T H T K H S H Q Q
       R Q R H T A E Q A H * R I Q N I P T N R
29221 - GAGCCTAAAAAGGACAAAAAGAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAA - 29280
    -EPKKDKKKKTDEAQPLPQRQ
    - S L K R T K R K R L M K L S L C R R D K - A * K G Q K E K D * * S S A F A A E T K
29281 - AAGAAGCAGCCCACTGTGACTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAA - 29340
    -KKQ PTVTLLPAADM D D F S R Q
    - R S S P L * L F F L R L T W M I S P D N
      EAAHCDSSSCG*HG*FLQTT
29341 - CTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATG - 29400
    -L Q N S M S G A S A D S T Q A * T L M M
    - FKIP * VELLLIQLRHKHS *
       SKFHEWSFC*FNSGINTHDD
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29401 - ACCACACAGGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTC - 29460
    -TTQGRWAM*TFSQFRLRYIV
    - P H K A D G L C K R F R N S V Y D T * S
    - H T R Q M G Y V N V F A I P F T I H S L
29461 - TACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTA - 29520
    - Y S C A E * I L V T K Q H K * V * L T L
    - T L V Q N E F S * L N S T S R F S * L *
    - LLCRMNSRN * TAQVGLVNFN
29521 - ATCTCACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCA - 29580
    -ISHSNL * SMCNIREDLKEPP
    - S H I A I F N Q C V T L G R T * K S H H
    - L T * Q S L I N V * H * G G L E R A T T
29581 - CATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG - 29640
    - H F H R G H A E Y D R G Y S E * C * G E
    - I F I E A T R S T I E G T V N N A R E S
    - FSSRPRGVRSRVQ*IMLGRA
29641 - CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG - 29700
    - L P I W K S P N V * N * F * * C Y P H V
    - C L Y G R A L M C K I N F S S A I P M *
    - AYMEEP * CVKLILVVLSPCD
- 29742
    -I L I A S * E N D K K K K X
    - F * * L L R R M T K K K X
    - FNSFLGE*QKKKX
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FIG. 11 Con't

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1 - TTTTTTTTTTTTTTTTTTTTTCCTAAGAAGCTATTAAAATCACATGGGGATAGCACTA - 60
  -FFFFVILLRSY*NHMGIAL
    FFFFLSFS*EAIKITWG*HY
     F F F F C H S P K K L L K S H G D S T T
61 - CTAAAATTAATTTTACACATTAGGGCTCTTCCATATAGGCAGCTCTCCCTAGCATTATTC - 120
  -LKLILHIRALPYRQLSLALF
    * N * F Y T L G L F H I G S S P * H Y S
     KINFTH * G S S I * A A L P S I I H
121 - ACTGTACCCTCGATCGTACTCCGCGTGGCCTCGATGAAAATGTGGTGGCTCTTTCAAGTC - 180
  -T V P S I V L R V A S M K M W W L F Q V
  - L Y P R S Y S A W P R * K C G G S F K S
     C T L D R T P R G L D E N V V A L S S P
181 - CTCCCTAATGTTACACATTGATTAAAGATTGCTATGTGAGATTAAAGTTAACTAAACCTA - 240
  -LPNVTH*LKIAM*D*S*LNL
    SLMLHID * RLLCEIKVN * TY
     P * C Y T L I K D C Y V R L K L T K P T
241 - CTTGTGCTGTTTAGTTACGAGAATTCATTCTGCACAAGAGTAGACTATGTATCGTAAACG - 300
  -L V L F S Y E N S F C T R V D Y V S * T
  - L C C L V T R I H S A Q E * T M Y R K R
     CAV*LREFILHKSRLCIVNG
301 - GAATTGCGAAAACGTTTACATAGCCCATCTGCCTTGTGTGGTCATCATGAGTGTTTATGC - 360
  -ELRKRLHSPSALCGHHECLC
  - N C E N V Y I A H L P C V V I M S V Y A
     I A K T F T * P I C L V W S S * V F M P
361 - CTGAGTTGAATCAGCAGAAGCTCCACTCATGGAATTTTGAAGTTGTCTGGAGAAATCATC - 420
  -LS * ISRSSTHGILKLSGEII
    * V E S A E A P L M E F * S C L E K S S
     E L N Q Q K L H S W N F E V V W R N H P
421 - CATGTCAGCCGCAGGAAGAAGAGTCACAGTGGGCTGCTTCTTTTGTCTCTGCGGCAAAGG - 480
  - H V S R R K K S H S G L L L L S L R Q R
   M S A A G R R V T V G C F F C L C G K G
     C Q P Q E E E S Q W A A S F V S A A K A
481 - CTGAGCTTCATCAGTCTTTTTCTTTTTGTCCTTTTTAGGCTCTGTTGGTGGGAATGTTTT - 540
  -LSFISLFLFVLFRLCWWECF
    * A S S V F F F L S F L G S V G G N V L
     ELHQSFSFCPF*ALLVGMFC
541 - GTATGCGTCAATGTGCTTGTTCAGCAGTATGACGTTGTCTTTGAATTGTGGATCTTTGTC - 600
  -V C V N V L V Q Q Y D V V F E L W I F V
  - Y A S M C L F S S M T L S L N C G S L S
     M R Q C A C S A V * R C L * I V D L C H
601 - ATCCAATTTAATGGCTCCATGATAAGTCAGCCATGTTCCCGAAGGTGTGACTTCCATGCC - 660
   -I Q F N G S M I S Q P C S R R C D F H A
   SNLMAP * * VSHVPEGVTSMP
     PI * W L H D K S A M F P K V * L P C Q
661 - AATGCGTGACATTCCAAAGAATGCAGAGGCACTTGGAGCAAATTGTGCAATTTGCGGCCA - 720
   -NA*HSKECRGTWSKLCNLRP
  - M R D I P K N A E A L G A N C A I C G Q
     CVTFQRMQRHLEQIVQFAAN
721 - ATGTTTGTAATCAGTTCCTTGTCTGATTAGGTCTTGGTCCCCGAAATTTCCTTGGGTTTG - 780
   -MFVISSLSD \star VLVPEISLGL
   C L * S V P C L I R S W S P K F P W V C
     V C N Q F L V * L G L G P R N F L G F V
781 - TTCTGGACCACGTCTCCCAAATGCTTGAGTGACGTTGTACTGTTTTGTGGCAGTACGTTT - 840
  -FWTTSPKCLSDVVLFCGSTF
  - S G P R L P N A * V T L Y C F V A V R F
    L D H V S Q M L E * R C T V L W Q Y V F
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841 - TTGGCGAGGCTTTTTAGATGCCTCAGCAGCAGATTTCTTAGTGACAGTTTGGCCTTGTTG - 900
   -LARLFRCLSSRFLSDSLALL
   - W R G F L D A S A A D F L V T V W P C C
       \texttt{G} \ \texttt{E} \ \texttt{A} \ \texttt{F} \ \texttt{*} \ \texttt{M} \ \texttt{P} \ \texttt{Q} \ \texttt{Q} \ \texttt{Q} \ \texttt{I} \ \texttt{S} \ \texttt{*} \ \texttt{*} \ \texttt{Q} \ \texttt{F} \ \texttt{G} \ \texttt{L} \ \texttt{V} \ \texttt{V} 
901 - TTGTTGGCCTTTACCAGAAACTTTGCTCTCAAGCTGGTTCAATCTGTCTAGCAGCAATAG - 960
   -LLAFTRNFALKLVQSV*QQ
   - C W P L P E T L L S S W F N L S S S N S
      V G L Y Q K L C S Q A G S I C L A A I A
961 - CGCGAGGGCAGTTTCACCACCTCCGCTAGCCATTCGAGCAGGAGAATTTCCCCTACTGCT - 1020
   -REGSFTTSASHSSRRISPTA
   - A R A V S P P P L A I R A G E F P L L L
      R G Q F H H L R * P F E Q E N F P Y C C
1021 - GCCAGGAGTTGAATTTCTTGAATTACCGCGACTACGTGATGAGGAGCGAGAAGAGGCTTG - 1080
   - A R S * I S * I T A T T * * G A R R G L
   - P G V E F L E L P R L R D E E R E E A *
      O E L N F L N Y R D Y V M R S E K R L D
1081 - ACTGCCGCCTCTGCTTCCCTCTGCGTAGAAGCCTTTTGGCAATGTTGTTCCTTGAGGAAG - 1140
   -TAASASLCVEAFWQCCSLRK
   - L P P L L P S A * K P F G N V V P * G S
      CRLCFPLRRSLLAMLFLEEV
1141 - TTGTAGCACGGTGGCAGCATTGTTATTAGGATTGCGGGTGCCAATGTGGTCTTTGGGTGT - 1200
   -L * H G G S I V I R I A G A N V V F G C
   - C S T V A A L L L G L R V P M W S L G V
      V A R W Q H C Y * D C G C Q C G L W V Y
1201 - ATTCAAGGCTCCCTCAGTTGCAACCCATACGATGCCTTCTTTGTTAGCGCCGTAGGGAAG - 1260
   -I Q G S L S C N P Y D A F F V S A V G K
   - F K A P S V A T H T M P S L L A P * G S
      S R L P Q L Q P I R C L L C * R R E V
1261 - TGAAGCTTCTGGGCCAGTTCCTAGGTAATAGAAGTACCATCTGGGGCTGAGCTCTTTCAT - 1320
   - * S F W A S S * V I E V P S G A E L F H
   - E A S G P V P R * * K Y H L G L S S F I
      K L L G Q F L G N R S T I W G * A L S F
1321 - TTTGCCGTCACCACCACGAACTCGTCGGGTAGCTCTTCGGTAGTAGCCAATTTGGTCATC - 1380
   -FAVTTTNSSGSSSVVANLVI
   - L P S P P R T R R V A L R * * P I W S S
      CRHHHELVG * LFGSSQFGHL
1381 - TGGACCACTATTGGTGTTGATTGGAACGCCCTGGCCTCGAGGGAATCTAAGTTCCTCCTT - 1440
   -W T T I G V D W N A L A S R E S K F L L
   - G P L L V L I G T P W P R G N L S S S L
      D H Y W C * L E R P G L E G I * V P P C
1441 - GCCATGCTGAGTGAGAGCTGTGAACCAAGACGCAGTATTATTGGGTAAACCTTGGGGTCG - 1500
    -AMLSESCEPRRSIIG*TLGS
    PC * V R A V N Q D A V L L G K P W G R
      1501 - GCGCTGTTTTGGCCTTGCCCCATTGCGTCCTCCATTCTGGTTATTGTCAGTTGAATCTGT - 1560
    -ALFWPCPIASSILVIVS * IC
    - R C F G L A P L R P P F W L L S V E S V
     A V L A L P H C V L H S G Y C Q L N L W
1561 - GGGTCCACCAAATGTAATGCGGGGGGCACTACGTTGGTTTGATTGGGGTCCATTATCAGA - 1620
    -G S T K C N A G G T T L V * L G S I I R
    - G P P N V M R G A L R W F D W G P L S D
      V H Q M * C G G H Y V G L I G V H Y Q T
1621 - CATTTTAATTTGTTCGTTTATTTAAAACAACAAGTACGTCTCTAAATGCAGCAGTTTGGT - 1680
   -H F N L F V Y L K Q Q V R L * M Q Q F G
    ILICSFI * NNKY V S K C S S L V
      F * F V R L F K T T S T S L N A A V W *
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1681 - GACCTTCATGAAGGTACCAACACCTAGCTATAAGCGCACCACCAGCTGGATCTTGACAGT - 1740
   -DLHEGTNT * L * A H H Q L D L D S
     T F M K V P T P S Y K R T T S W I L T V
      PS * RYQHLAISAPPAGS * QL
1741 - TGATAGTAACATTAGGTGTGCATGTTTGAACCATAGTGTGCCATCTATGAAAAGGTAAAA - 1800
   - * * * H * V C M F E P * C A I Y E K V K
   - D S N I R C A C L N H S V P S M K R * N
     I V T L G V H V * T I V C H L * K G K T
1801 - CCTTTCCTAGAGCACAAGCCAAGCAGTGCTATAAGTATTACCCCTAGTGTTGTACCTTA - 1860
   -PFLEHKAKQCYKYYP*CCTL
   - L S * S T K P S S A I S I T P S V V P Y
      F P R A Q S Q A V L * V L P L V L Y L T
1861 - CAAGGATCTTCAAGCACATGAGGTTTATTAGATGCACAGCGCTGTACTACAGTGCATATG - 1920
   - O G S S S T * G L L D A Q R C T T V H M
   - K D L Q A H E V Y * M H S A V L Q C I C
      RIFKHMRFIRCTALYYSAYA
1921 - CAACTGCATAGAGAAATACAAGTCAAAACAATGAGAAGTTTCATGTTCGTTTAGACTTTG - 1980
   -Q L H R E I Q V K T M R S F M F V * T L
   - N C I E K Y K S K Q * E V S C S F R L W
      TA*RNTSQNNEKFHVRLDFG
1981 - GTACAAGGTTCTTCTAGATCCTGGATTTCGAGTGAAAACCAAAATATAATAAGCATTATT - 2040
   -V Q G S S R S W I S S E N Q N I I S I I
   - Y K V L L D P G F R V K T K I * * A L L
      TRFF*ILDFE*KPKYNKHY*
2041 - AAAACAAGGAATAGCAGAAAGGCTAAAAAGCACAAATAGAAGTCAATTAAAGTGAGCTCA - 2100
   -KTRNSRKAKKHK*KSIKVSS
   - K Q G I A E R L K S T N R S Q L K * A H
      NKE * QKG * KAQIEVN * SELI
2101 - TTCATTCTGTCTTTCTCTTAATGGTGAAGCAAAGTATTAAAAATACTAGAGCAGCAACAA - 2160
   -FILSFS * W * S K V L K I L E Q Q Q
   - S F C L S L N G E A K Y * K Y * S S N N
      H S V F L L M V K Q S I K N T R A A T M
2161 - TGAGAAAAGTGGCGAGTAGAGCTCTTGTTGAACCTCCTCTTGTCTGATGAAAAGTTTTG - 2220
   - * E K V A S R A L V E P P L V * * K V L
    E K K W R V E L L N L L S D E K F W
     R K S G E * S S C * T S S C L M K S F G
2221 - GTGAAACTGATCTTGCACGCAGCTGATAGGTATGTCGAGTACCGTCAGCACAAGCAAAAG - 2280
   -V K L I L H A A D R Y V E Y R Q H K Q K
     * N * S C T Q L I G M S S T V S T S K S
E T D L A R S * * V C R V P S A Q A K A
2281 - CAAAGTGTGTGCTAGTGCAAGTTAGTGCAAATTTATTGTCAGCAAGAGGGTGAAATGGTG - 2340
   -QSVC * CKLVQIYCQQEGEMV
    KVCASAS * CKFIVSKRVKW *
      K C V L V Q V S A N L L S A R G * N G E
2341 - AATTGCCCTCGTATGTTCCTGATGGCCAAGGTTCTTTTAGTAGTACAGTCGTACCTCTAA - 2400
   -NCPRMFLMGKVLLVVQSYL*
     I A L V C S * W A R F F * * Y S R T S N
     L P S Y V P D G Q G S F S S T V V P L T
-HTPDSDIARKM*IQSMSGRE
     T L L I V I * L A R C K Y N Q C Q E E N
     HS***YSSQDVNTINVRKRI
2461 - TAATTTTCATGTTCGTTTTATGGATAATCTAACTCCATAGGTTCTTCATCATCTAACTCC - 2520
   - * F S C S F Y G * S N S I G S S S N S
    N F H V R F M D N L T P * V L H H L T P
      IFMFVLWII*LHRFFII*LR
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2521 - GAATAATTCTTCTTAGTTAGAGGCTTAAATAATTGTCTCACTATTGAACTTATTATAACG - 2580
   -E * F F L V R G L N N C L T I E L I I T
   - N N S S * L E A * I I V S L L N L L * R
      I I L L S * R L K * L S H Y * T Y Y N V
2581 - TCAAGATTCCAAATAGCAATCCTGAAAGTCCTCATAATGATAATCAATATCTCTGCTATT - 2640
   -S R F Q I A I L K V L I M I I N I S A I
   - Q D S K * Q S * K S S * * * S I S L L L
      K I P N S N P E S P H N D N Q Y L C Y C
2641 - GTAACCTGGAAGTCAACAAGATGAAACATCTGTTGTCACTTACTGTACTAGCAAAGCAAT - 2700
   -V T W K S T R * N I C C H L L Y * Q S N
     * P G S Q Q D E T S V V T Y C T S K A I
      N L E V N K M K H L L S L T V L A K Q Y
2701 - ATTGTCGTTGCTACCGGCGTGGTCTGTATTTAATTTATAGTTTCCAATACGGTAGCGGTT - 2760
   -I V V A T G V V C I * F I V S N T V A V
   - L S L L P A W S V F N L * F P I R * R L
     C R C Y R R G L Y L I Y S F Q Y G S G C
2761 - GTATGCAGCAAAACCTGAATCAGTGCCTACACGCTGCGACGCTCCTAATTTGTAATAAGA - 2820
   -V C S K T * I S A Y T L R R S * F V I R
   - Y A A K P E S V P T R C D A P N L * * E
      M Q Q N L N Q C L H A A T L L I C N K K
2821 - AAGCGTTCGTGATGTAGCCACAGTGATCTCTTTTGGCAGGTCCTTAATGTCACAGCGCCC - 2880
   -KRS * C S H S D L F W Q V L N V T A P
   - S V R D V A T V I S F G R S L M S Q R P
      A F V M * P Q * S L L A G P * C H S A L
2881 - TAGGGAGTGTCCGGCCATTCGCAAGTGACCACGAATGATCACAGCACCAATGACAAGTTC - 2940
   - * G V S G H S Q V T T N D H S T N D K F
   - RECPAIRK* PRMITAPMTS S
     GSVRPFASDHE*SQHQ*QVH
2941 - ACTTTCCATGAGCGGTCTGGTCACAATTGTCCCCCGGAGAGGCACATTGAGAAGAATGTT - 3000
   -TFHERSGHNCPPERHIEKNV
   - L S M S G L V T I V P R R G T L R R M F
      FP*AVWSQLSPGEAH*EECL
-C F W V E * P H * A G T S K Q P E G S N
   - V S G L N D H I E R V R A N S L K E A T
   - FLG * M T T L S G Y E Q T A * R K Q R
3061 - GAAGTAGCTAAGCCACATCAAGCCTACAATACAAGCCATTGCAATCGCAATCCCGCCAGT - 3120
   -EVAKPHQAYNTSHCNRNPAS
   - K * L S H I K P T I Q A I A I P P V
     S S * A T S S L Q Y K P L Q S Q S R Q S
- H P I N S V D N S K H K T S K C Y W P Q
   - TQLIL * T T A S T K Q A S V T G H K
     PN * FCROOOAONKQVLLATR
3181 - GAGCCAGAGGAAAACAAGCTTTATTATGTACAAAAACCTGTTCCGATTAGAATAGGCAAA - 3240
   -EPEENKLYYVQKPVPIRIGK
   - S Q R K T S F I M Y K N L F R L E * A N
      ARGKQALLCTKTCSD*NRQI
3241 - TTGTAGTAACATAATCCAGGCTAGGAATAGGAAACCTATTACTAGGTTCCATTGTTCCAG - 3300
   -L * * H N P G * E * E T Y Y * V P L F Q
   - C S N I I Q A R N R K P I T R F H C S R
     V V T * S R L G I G N L L L G S I V P G
3301 - GAGTTGTTTAAGCTCCTCAACGGTAATAGTACCGTTGTCTGCCATGATAAGCAATGTTAA - 3360
   -ELFKLLNGNSTVVCHDKQC *
   - S C L S S S T V I V P L S A M I S N V K
      V V * A P O R * * Y R C L P * * A M L K
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3361 - AGTTCCAAACAGAATAATAATAATAGTTAGTTCGTTTAGACCAGAAGATCAGGAACTCCT - 3420
   - V P N R I I I I V S S F R P E D Q E L L
      FOTE****LVRLDQKIRNSF
3421 - TCAGAAGAGTTCAGATTTTTAACACGCGAGTAGACGTAAACCGTTGGTTTTACTAAACTC - 3480
   -SEEFRFLTRE*T*TVGFTKL
   - Q K S S D F * H A S R R K P L V L L N S
      RRVQIFNTRVDVNRWFY*TH
3481 - ACGTTAACAATATTGCAGCAGTACGCACACAATCGAAGCGCAGTAAGGATGGCTAGTGTG - 3540
   -TLTILQQYAHNRSAVRMASV
     R * Q Y C S S T H T I E A Q * G W L V *
      V N N I A A V R T Q S K R S K D G * C D
3541 - ACTAGCAAGAATACCACGAAAGCAAGAAAAAGAAGTACGCTATTAACTATTAACGTACCT - 3600
   -TSKNTTKARKRSTLLTINVP
    LARIPRKQEKEVRY*LLTYL
      * Q E Y H E S K K K K Y A I N Y * R T C
3601 - GTTTCTTCCGAAACGAATGAGTACATAAGTTCGTACTCACTTTCTTGTGCTTACAAAGGC - 3660
   -V S S E T N E Y I S S Y S L S C A Y K G
   - F L P K R M S T * V R T H F L V L T K A
     FFRNE * V H K F V L T F L C L Q R H
3661 - ACGCTAGTAGTCGTCGGCTCATCATAAATTGGATCCATTGCTGGATTAGCAACTCCT - 3720
   - T L V V V G S S * I G S I A G L A T P
   - R * * S S S A H H K L D P L L D * Q L L
    ASSRRRLIINWIHCWISNS*
3721 - GAAGAGCCGTCGATTGTGTATTTGCACATTCGGTGGGTCTTTAACAAGCTTGTTAAAG - 3780
   -EEPSIVCICTFGGSLTSLLK
   - K S R R L C V F A H S V G L * Q A C * R
      R A V D C V Y L H I R W V F N K L V K D
3781 - ATGAAGAATGTAGCATTTTCAATACCAGTGTCTGTAGTAATTTGTGTAGACTCAAGCTGG - 3840
   - M K N V A F S I P V S V V I C V D S S W
     * R M * H F Q Y Q C L * * F V * T Q A G
      E E C S I F N T S V C S N L C R L K L V
3841 - TAGTAAACTTCGGTGAAATAGCCATGTACAACGACATAGTCTTTAACACCTGAGTGCCTA - 3900
   - * * T S V K * P C T T T * S L T P E C L
   - S K L R * N S H V Q R H S L * H L S A Y
     VNFGEIAMYNDIVFNT * VPI
3901 - TCCTCAGAATAACCACCAATTTGGTAGTCTTCTTTGAGTTTTTGGTGTTGAAATGCCGTCA - 3960
   -SSE*PPIW*SSLSFGVEMPS.
   - P O N N H Q F G S L L * V L V L K C R H
     LRITTNLVVFFEFWC*NAVT
3961 - CCTTCAGTAACGACAATTGTATCTGTGACACTGTTATATGGTATACAGTAGTCATAGTTA - 4020
   -PSVTTIVSVTLLYGIQ*S*L
   - L O * R O L Y L * H C Y M V Y S S H S Y
   - F S N D N C I C D T V I W Y T V V I V M
4021 - TGTGTGTGCCAGCAAACAAGTAGTTGGCATCATAAAGTAATGGGTTCTTGGATTTGCAC - 4080
   -C V C Q Q T K * L A S * S N G F L D L H
    V C A S K Q S S W H H K V M G S W I C T
      C V P A N K V V G I I K * W V L G F A L
4081 - TTCCAACAAGCCAACATCTCATAATAATTCTACATGCGTTGATGCATTGTAGAAAATAT - 4140
   - F Q Q S Q H L I I I L H A L M H C R K Y - S N K A N I S * * F Y M R * C I V E N I
     PTKPTSHNNSTCVDAL*KIY
4141 - ATCAAGGCATAGAGGTACAAAAATTGCGCCTCCTTACCTGCAGCGACAAGCAAAAGATGT - 4200
   -I K A * R Y K N C A S L P A A T S K R C
    S R H R G T K I A P P Y L Q R Q A K D V
      Q G I E V Q K L R L L T C S D K Q K M *
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4201 - GAATAGATGGTAACAAATAGCAGCAGTAAATTGCAAATGAACTGGAAGCCCTTATAAAGG - 4260
    -E * M V T N S S S K L Q M N W K P L * R
   - N R W * Q I A A V N C K * T G S P Y K G
      I D G N K * Q Q * I A N E L E A L I K G
4261 - GCTAGCTGCCATCTTTTATTGAGCGCAATTATTTTGGTAGCGCTCTGAAAAACAGCAAGA - 4320
    -ASCHLLLSAIILVAL*KTAR
   - L A A I F Y * A Q L F W * R S E K Q Q E
      * L P S F I E R N Y F G S A L K N S K K
4321 - AATGCAACGCCAATAACAAGCCATCCGAAAGGGAGTGAGGCTTGTAGCGGTATCGTTGCT - 4380
    -NATPITSHPKGSEACSGIVA
     M Q R Q * Q A I R K G V R L V A V S L L
       C N A N N K P S E R E * G L * R Y R C C
4381 - GTAGCATGAACAGTACTTGCAGGAGAAGCATTGTCAATTTTTACTGGCTGTGCAGTAATT - 4440
    -VA * T V L A G E A L S I F T G C A V I
     * H E Q Y L Q E K H C Q F L L A V Q * L
       S M N S T C R R S I V N F Y W L C S N *
4441 - GATCCAAGAGTAAAAAATCTCATAAACAAATCCATAAGTTCGTTTATGTGTAATGTAATT - 4500
    - D P R V K N L I N K S I S S F M C N V I
     I Q E * K I S * T N P * V R L C V M * F
      SKSKKSHKQIHKFVYV * CNL
4501 - TGACACCCTTGAGAACTGGCTCAGAGTCATCCTCATCAAACTTGCAGCAAGAACCACAAG - 4560
    - * H P * E L A Q S H P H Q T C S K N H K
     D T L E N W L R V I L I K L A A R T T R
       \texttt{T} \  \, \texttt{P} \  \, \texttt{L} \  \, \texttt{R} \  \, \texttt{T} \  \, \texttt{G} \  \, \texttt{S} \  \, \texttt{E} \  \, \texttt{S} \  \, \texttt{S} \  \, \texttt{S} \  \, \texttt{N} \  \, \texttt{L} \  \, \texttt{Q} \  \, \texttt{Q} \  \, \texttt{E} \  \, \texttt{P} \  \, \texttt{Q} \  \, \texttt{E} 
4561 - AGCATGCACCCTTGAGGCAACTGCAACAACTAGTCATGCAACAAAGCAAGATTGTAACCA - 4620
    - S M H P * G N C N N * S C N K A R L * P
    - A C T L E A T A T T S H A T K Q D C N H
     HAPLRQLQQLVMQQSKIVT M
4621 - TGACGATGGCAATTAGTCCAGCAATGAAGCCGAGCCAAACATACCAAGGCCATTTAATAT - 4680
    - * R W Q L V Q Q * S R A K H T K A I * Y
     D D G N * S S N E A E P N I P R P F N I
      T M A I S P A M K P S Q T Y Q G H L I Y
4681 - ATTGCTCATATTTTCCCAATTCTTGAAGGTCAATGAGTGATTCATTTAAATTTTTAGCGA - 4740
    -IAHIFPILEGQ * VIHLNF * R
     L L I F S Q F L K V N E * F I * I F S D C S Y F P N S * R S M S D S F K F L A T
4741 - CCTCATTGAGGCGGTCAATTTCTTTTTGAATGTTGACGACAGAAGCGTTAATGCCTGAAA - 4800
    LIEAVNFFLNVDDRSVNA*N
     S L R R S I S F * M L T T E A L M P E M
4801 - TGTCGCCAAGATCAACATCTGGTGATGTATGATTTTTGAAGTACTTGTCCAGCTCTTCTT - 4860
    -CRQDQHLVMYDF*STCPALL
     V A K I N I W * C M I F E V L V Q L F F
       S P R S T S G D V * F L K Y L S S S S L
4861 - TGAATGAGTCAAGCTCAGGTTGCAGAGGATCATAAACTGTGTTGTTAATGATGCCAATAA - 4920
    - * M S Q A Q V A E D H K L C C * * C Q *
     E * V K L R L Q R I I N C V V N D A N N
       NESSSGCRGS*TVLLMMPIT
4921 - CGACATCACAATTTCCTGAGACAAATGTATTGTCTGTAGTAATTATTTGTGGAGAAAAGA - 4980
    -RHHNFLRQMYCL**LFVEKR
     DITIS * D K C I V C S N Y L W R K E
      T S Q F P E T N V L S V V I I C G E K K
4981 - AGTTCCTCTGTGTAATAAACCAAGAAGTGCCATTAAACACAAAAACACCTTCACGAGGGA - 5040
    V P L C N K P R S A I K H K N T F T R E
       F L C V I N Q E V P L N T K T P S R G K
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5041 - AGTATGCTTTGCCTTCATGACAAATTGCTGGCGCTGTGGTGAAGTTCCTCTCCTGGGATG - 5100
   - S M L C L H D K L L A L W * S S P G M
    V C F A F M T N C W R C G E V P L L G W
     Y A L P S * Q I A G A V V K F L S W D G
5101 - GCACATACGTGACATGTAGGAAGACAACACCATGCGGGGCTGCTTGTGGGAAGGACATAA - 5160
   -AHT*HVGRQHHAGLLVGRT*
    HIRDM*EDNTMRGCLWEGHK
      TYVTCRKTTPCGAACGKDIR
5161 - GGTGGTAGCCCTTTCCACAAAAGTCAACTCTTTTTGATTGTCCAAGAACACACTCAGACA - 5220
   -GGSPFHKSQLFLIVQEHTQT
     V V A L S T K V N S F * L S K N T L R H
     W * P F P Q K S T L F D C P R T H S D I
5221 - TTTTAGTAGCAGCAAGATTAGCAGAAGCCCTGATTTCAGCAGCCCTGATTAGTTGTTGTG - 5280
   -F * * Q Q D * Q K P * F Q Q P * L V V V
   - FSSSKISRSPDFSSPD * LLC
     LVAARLAEALISAALISCCV
5281 - TTACATAGGTTTGAAGGCTTTGAAGTCTGCCTGTAATTAACCTGTCAATTTGTACCTCCG - 5340
   -LHRFEGFEVCL*LTCQFVPP
    Y I G L K A L K S A C N * P V N L Y L R
      T * V * R L * S L P V I N L S I C T S A
5341 - CCTCGACTTTATCAAGTCGCGAAAGGATATCATTTAGCACACTTGAAATTGCACCAAAAT - 5400
   -PRLYQVAKGYHLAHLKLHQN
    LDFIKSRKDII*HT*NCTKI
     STLSSRERISFSTLEIAPKL
5401 - TAGAGCTAAGTTGTTTAACAAGTGTGTTTAATGCTTGAGCATTCTGGTTAACAACGTCTT - 5460
   - * S * V V * Q V C L M L E H S G * Q R L
    RAKLFNKCV * CLSILVNNVL
     ELSCLTSVFNA*AFWLTTSC
5461 - GCAGCTTGCCCAATGCAGTTGATGTTGTTGTAAGTGATTCTTGAATTTGACTAATCGCCT - 5520
   -AACPMQLMLL * VILEFD * SP
    Q L A Q C S * C C C K * F L N L T N R L
S L P N A V D V V V S D S * I * L I A L
5521 - TGTTAAATTGGTTGGCGATTTGTTTTTGGTTCTCATAGAGAACATTTTGGGTAACTCCAA - 5580
   -C * I G W R F V F G S H R E H F G * L Q
    V K L V G D L F L V L I E N I L G N S N
     LNWLAICFWFS*RTFWVTPM
5581 - TGCCATTGAACCTATATGCCATTTGCATAGCAAAAGGTATTTGAAGAGCAGCGCCAGCAC - 5640
   -C H * T Y M P F A * Q K V F E E Q R Q H
    A I E P I C H L H S K R Y L K S S A S T
P L N L Y A I C I A K G I * R A A P A P
5641 - CAAATGTCCATCCAGCAGTGCCAGTACCACTAACTAGAGCAGCAGTGTAGGCAGCAATCA - 5700
   -QMSIQQWQYH*LEQQCRQQS
    KCPSSSGSTTN*SSSVGSNH
     N V H P A V A V P L T R A A V * A A I I
5701 - TATCATCAGTGAGCAGAGGTGGCAACACTGTAAGTCCATTGAACTTCTGCGCACAAATGA - 5760
   I I S E Q R W Q H C K S I E L L R T N E
     S S V S R G G N T V S P L N F C A Q M R
5761 - GATCTCTAGCATTAATATCACCTAGGCATTCGCCATATTGCTTCATGAAGCCAGCATCAG - 5820
   -DL * H * Y H L G I R H I A S * S Q H Q
    ISSINIT * A F A I L L H E A S I S
     S L A L I S P R H S P Y C F M K P A S A
5821 - CGAGTGTCACCTTATTAAAGAGCAAGTCCTCAATAAAAGACCTCTTAGTTGGCTTTAGAG - 5880
   -RVSPY*RASPQ*KTS*LALE
    ECHLIKEQVLNKRPLSWL*R
      S V T L L K S K S S I K D L L V G F R G
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5881 - GGTCAGGTAATATTTGTGAAAAATTAAAACCACCAAAATATTTCAAAGTTGGGGTTTTGT - 5940
   -G Q V I F V K N * N H Q N I S K L G F C
     V R * Y L * K I K T T K I F Q S W G F V
      SGNICEKLKPPKYFKVGVLY
5941 - ACATTTGTTTGACTTGAGCGAACACTTCACGTGTGTTGCGATCCTGTTCAGCAGCAATAC - 6000
   - T F V * L E R T L H V C C D P V Q Q Q Y
   - H L F D L S E H F T C V A I L F S S N T
      ICLT * ANTSRVLRSCSAAIP
6001 - CTGAGAGTGCACGATTTAGTTGTGTGCAAAAGCTACCATATTGGAGAAGCAAATTAGCAC - 6060
   -LRVHDLVVCKSYHIGEAN*H
     * E C T I * L C A K A T I L E K Q I S T
      E S A R F S C V Q K L P Y W R S K L A H
6061 - ATTCAGTAGAATCTCCGCAGATGTACATATTACAATCTACGGAGGTTTTAGCCATAGAAA - 6120
   -IQ * N L R R C T Y Y N L R R F * P * K
    F S R I S A D V H I T I Y G G F S H R N
      S V E S P Q M Y I L Q S T E V L A I E T
6121 - CAGGCATTACTTCTGTAGTAATGCTAATTGAAAAGTTAGTAGGTATAGCAATGGTGTTAT - 6180
   -O A L L L * * C * L K S * * V * Q W C Y
    R H Y F C S N A N * K V S R Y S N G V I
      G I T S V V M L I E K L V G I A M V L L
6181 - TAGAGTAAGCAATTGAACTATCAGCACCTAAAGACATAGTATAAGCCACAATAGATTTTT - 6240
   - * S K Q L N Y Q H L K T * Y K P Q * I F
    R V S N * T I S T * R H S I S H N R F L
     E * A I E L S A P K D I V * A T I D F W
6241 - GGCTAGTACTACGTAATAAAGAAACTGTATGGTAACTAGCACAAATGCCAGCTCCAATAG - 6300
   -G * Y Y V I K K L Y G N * H K C Q L Q *
     A S T T * * R N C M V T S T N A S S N R
     L V L R N K E T V W * L A Q M P A P I G
6301 - GAATGTCGCACTCATAAGAAGTGTCGACATGCTCAGCTCCTATAAGACAGCCTGCTTGAG - 6360
   -E C R T H K K C R H A Q L L * D S L L E
     N V A L I R S V D M L S S Y K T A C L S
      M S H S * E V S T C S A P I R Q P A * V
6361 - TCTGGAATACATTGTTTCCAGTAGAATATATGCGCCAAGCTGGTGTGAGTTGATCTGCAT - 6420
   -SGIHCFQ * NICAKLV * V D L H
     LEYIVSSRIYAPSWCELICM
      W N T L F P V E Y M R Q A G V S * S A
6421 - GAATTGCTGTAGAAACATCAGTGCAGTTAACATCTTGATATAGAACAGCAACTTCAGATG - 6480
   -ELL * K H Q C S * H L D I E Q Q L Q M
     N C C R N I S A V N I L I * N S N F R *
      I A V E T S V Q L T S * Y R T A T S D E
6481 - AAGCATTTGTTCCAGGTGTAATTACACTTACACCCCCAAAAGAGCAAGGTGAAATGTCTA - 6540
   -K H L F Q V * L H L H P Q K S K V K C L
     SICSRCNYTYTPKRAR*NV*
     A F V P G V I T L T P P K E Q G E M S N
6541 - ATATTTCAGATGTTTTAGGATCTCGAACGGAATCAGTGAAATCAGAAACATCACGGCCAA - 6600
   - I F Q M F * D L E R N Q * N Q K H H G Q
     Y F R C F R I S N G I S E I R N I T A K
      I S D V L G S R T E S V K S E T S R P N
6601 - ATTGTTGAAATGGTTGAAATCTCTTTGAAGAAGGAGTTAACACACCAGTACCAGTGAGTC - 6660
    -IVEMVEISLKKELTHQYQ*V
     L L K W L K S L * R R S * H T S T S E S
     C * N G * N L F E E G V N T P V P V S P
6661 - CATTAAAATTAAAATTGACACACTGGTTCTTAATAAGGTCAGTGGATAATTTTGGTCCAC - 6720
    - H * N * N * H T G S * * G Q W I I L V H
     IKIKIDTLVLNKVSG*FWST
      LKLKLTHWFLIRSVDNFGPQ
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6721 - AAACCGTGGCCGGTGCATTTAAAAGTTCAAAAGAAAGTACTACAACTCTGTAAGGTTGGT - 6780
   -KPWPVHLKVQKKVLQLCKVG
     N R G R C I * K F K R K Y Y N S V R L V
     T V A G A F K S S K E S T T T L * G W
6781 - AGCCAATGCCAGTAGTGGTGTAAAAACCATAATCATTTAATGGCCAATAACAATTAAGAG - 6840
   -SQCQ*WCKNHNHLMANNN*E
    A N A S S G V K T I I I * W P I T I K S
      PMPVVV*KP*SFNGQ*QLRA
6841 - CAGGTGGGGTGCAAGGTTTGCCATCAGGGGAGAAAGGCACATTAGATATGTCTCTCAA - 6900
   -Q V G C K V C H Q G R K A H * I C L S Q
     R W G A R F A I R G E R H I R Y V S L K
      G G V Q G L P S G E K G T L D M S L S K
-RA * A C H V * D T Y I Y N Y N Y Q L K
    GPKLAMSKIPIFIIIITS*S
      G L S L P C L R Y L Y L * L P V E V
6961 - TAGCATCAATGTTCCTAGTATTCCAAGCAAGGACACCCATGAAATCATCTGGCAATT - 7020
   - * H Q C S * Y S K Q G H N P * N H L A I
     SINVPSIPSKDTTHEIIWQF
      A S M F L V F Q A R T Q P M K S S G N L
7021 - TATAATTATAATCAGCAATAACACCAGTTTGTCCTGGCGCTATTTGTCTTACATCATCTC - 7080
   -YNYNQQ*HQFVLALFVLHHL
     I I I I S N N T S L S W R Y L S Y I I S
     * L * S A I T P V C P G A I C L T S S P
7081 - CCTTGACTACAAAAGAATCTGCATAGACATTGGAGAAGCAAAGATCATTCAACTTAGTGG - 7140
   -P * L Q K N L H R H W R S K D H S T * W
    LDYKRICIDIGEAKIIQLSG
      L T T K E S A * T L E K Q R S F N L V A
7141 - CAGAAACGCCATAGCACTTAAAGGTTGAAAAAAATGTTGAGTTGTAGAGCACAGAGTAAT - 7200
   -QKRHST*RLKKMLSCRAQSN
     R N A I A L K G * K K C * V V E H R V I
      ETP*HLKVEKNVEL*STE*S
7201 - CAGCAACACAATTAGAAATTTTTTTTTCTCCCATGCATAGACAGAAGGGAATTTAGTAG - 7260
   -QQHN*KFFFSPMHRQKGI**
     SNTIRNFFSLPCIDRREFSS
     A T Q L E I F F L S H A * T E G N L V A
7261 - CATTAAAAACCTCTCCAAAAGGACACAAGTTTGTAATATTAGGGAATCTCACAACATCTC - 7320
   - H * K P L Q K D T S L * Y * G I S Q H L
    I K N L S K R T Q V C N I R E S H N I S
     LKTSPKGHKFVILGNLTTSP
7321 - CTGAGGGAACAACCCTGAAATTAGAGGTCTGGTAAATTCCTTTGTCAATCTCAAAGCTCT - 7380
   -L R E Q P * N * R S G K F L C Q S Q S S
      GNNPEIRGLVNSFVNLKAL
      EGTTLKLEVW*IPLSISKLL
7381 - TAACAGAGCATTTGAGTTCAGCAAGTGGATTTTGAGAACAATCAACAGCATCTGTGATTG - 7440
   - * Q S I * V Q Q V D F E N N Q Q H L * L
     N R A F E F S K W I L R T I N S I C D C T E H L S S A S G F * E Q S T A S V I V
7441 - TACCATTTTCATCATACTTGAGCATAAATGTAGTTGGCTTTAAATAGCCAACAAAATAGG - 7500
   -YHFHHT * A * M * L A L N S Q Q N R
     TIFIILE H K C S W L * I A N K I G
     PFSSYLSINVVGFK*PTK*A
7501 - CTGCAGCTGACGTGCCCCAAATGTCTTGAGCAGGTGAAAAGGCTGTAAGAATGGCTCTAA - 7560
   -LQLTCPKCLEQVKRL*EWL*
   - C S * R A P N V L S R * K G C K N G S K
     A A D V P Q M S * A G E K A V R M A L K
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7561 - AATTTGTAATGTTAATACCAAGAGGCAACTTAAAAATAGGTTTCAAAGTGTTAAAACCAG - 7620
   - N L * C * Y Q E A T * K * V S K C * N Q
   - I C N V N T K R Q L K N R F Q S V K T R
      F V M L I P R G N L K I G F K V L K P E
7621 - AAGGTAGATCACGAACTACATCTATAGGTTGATAGCCCTTATAAACATAGAGAAACCCAT - 7680
   -KVDHELHL*VDSPYKHRETH
   - R * I T N Y I Y R L I A L I N I E K P I
     GRSRTTSIG**PL*T*RNPS
7681 - CTTTATTTTTAAACACAAACTCTCGTAAGTGTTTAAAATTACCTGACTTTTCTGAAACAT - 7740
   -LYF*TQTLVSV*NYLTFLKH
   - FIFKHKLS * V FKIT * L F * N I
     L F L N T N S R K C L K L P D F S E T S
7741 - CAAGCGAAAAGGCATCAGATATGTACTCGAAAGTGCAATTAAATGCATTATCGAATATCA - 7800
   -QAKRHQICTRKCN * MHYRIS
   - K R K G I R Y V L E S A I K C I I E Y H
      S E K A S D M Y S K V Q L N A L S N I I
- * Y V S V Y P W V * K Q Q R K G C H T I
    S M C L C T H G F R N S K E R V V T Q F
      V C V C V P M G L E T A K K G L S H N S
7861 - CAAAGTTACATGCTCGTATAACAACATTAGTAGAATTGTTAATAATAATCACCGACTGTG - 7920
   - Q S Y M L V * Q H * * N C * * * S P T V
   - KVTCSYNNISRIVNNNHRL*
      K L H A R I T T L V E L L I I T D C D
7921 - ACTTGTTGTTCATGGTAGAACCAAAAACCCAACCACGGACAACATTTGATTTCTCTGTGG - 7980
   -T C C S W * N Q K P N H G Q H L I S L W
   - L V V H G R T K N P T T D N I * F L C G
     LLFMVEPKTQPRTTFDFSVA
7981 - CAGCAAATAAATACCATCCTTAAAAGGTATGACAGGGTTGCCAAACGTATGATTAATAG - 8040
   - O O N K Y H P * K V * Q G C Q T Y D * *
   - S K I N T I L K R Y D R V A K R M I N S
     AK*IPSLKGMTGLPNV*LIV
-YETL*H*NKMEEINPELNKE
    M K P C N I R I K W K K * I L S * I K S
     * N P V T L E * N G R N K S * V K * R V
8101 - TGTCTGATCTAAAAATTTCATCAGGATAGTAAACCCCCCTCATAGATGAAGTATGTTGAG - 8160
   -CLI*KFHQDSKPPS*MKYVE
    V * S K N F I R I V N P P H R * S M L S
S D L K I S S G * * T P L I D E V C * V
8161 - TGTAATTAGGAGCTTGAACATCATCAAAAGTGGTGCACCGGTCAAGGTCACTACCACTAG - 8220
   -C N * E L E H H Q K W C T G Q G H Y H *
    VIRSLNIIKSGAPVKVTTTS
     * L G A * T S S K V V H R S R S L P L V
8221 - TGAGAGTAAGAAATAATAAGAAAATAAACATGTTCGTTTAGTTGTTAACAAGAATATCAC - 8280
   - * E * E I I R K * T C S F S C * Q E Y H
    ESKK**ENKHVRLVVNKNIT
      R V R N N K K I N M F V * L L T R I S L
8281 - TTGAAACCACACTCTGTTGTTTTCTCTAATGATAAGCCTACCTTTTTCCAGAAGAGAAT - 8340
   -LKPQLCCFL***AYLFPEEN
      N H N S V V F S N D K P T F F Q K R I
      ETTTLLFSLMISLPFSRRE*
8341 - AAATCATATCATTGATTTGATTCTCCTTAAGAGACATTACAGCAGTTCCTCTTAATTTAA - 8400
   -KSYH*FDSP*ETLQQFLLI*
    N H I I D L I L L K R H Y S S S S * F K
      I I S L I * F S L R D I T A V P L N L R
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8401 - GAGGAAATTTGCTCATGTCAAAGAGTGAATAGGAAGACAACTGGATAGGATTTGTGTTCC - 8460
   -EEICSCQRVNRKTTG * D L C S
   - R K F A H V K E * I G R Q L D R I C V P
      G N L L M S K S E * E D N W I G F V F L
8461 - TCCAGAAAATGTAGTTAGCATGCATGGTATAGCCATCAATTTGTTCCTTCGGCTTGCCAA - 8520
   -SRKCS*HAWYSHQFVPSACQ
    PENVVSMHGIAINLFLRLAK
      Q K M * L A C M V * P S I C S F G L P R
8521 - GATAGTTAGCCCCAATTAAAAATGCTTCCGATGATGATGCATTTACATTTGTAACAAAAG - 8580
   -DS * PQ L K M L P M M M H L H L * Q K
     I V S P N * K C F R * * C I Y I C N K S
     * L A P I K N A S D D D A F T F V T K A
8581 - CTGTCCACCATGAGAAATGGCCCATAAGCTTGTAAAGGTCAGCATTCCAAGAATGCTCTG - 8640
   -L S T M R N G P * A C K G Q H S K N A L
   - C P P * E M A H K L V K V S I P R M L C
     V H H E K W P I S L * R S A F Q E C S V
8641 - TTATCTTTACAGCTATAGAACCACCCAGGGCTAGTTTTTGCTTTATAAATCCACACAGAT - 8700
   -L S L Q L * N H P G L V F A L * I H T D
   - Y L Y S Y R T T Q G * F L L Y K S T Q I
      IFTAIEPPRASFCFINPHR*
8701 - AAGTGAAAAACCCTTCTTTAGAGTCATTCTCTTTTGTCACATGTTTGGTCCTAGGGTCAT - 8760
   -K * K T L L * S H S L L S H V W S * G H
   - S E K P F F R V I L F C H M F G P R V I
     V K N P S L E S F S F V T C L V L G S Y
8761 - ACATATCGCTAATAATAAGGTCCCATTTATTAGCCGTATGTACTGTTGCACAGTCTCCAA - 8820
   - T Y R * * * G P I Y * P.Y V L L H S L Q
   - H I A N N K V P F I S R M Y C C T V S N
      I S L I I R S H L L A V C T V A Q S P I
8821 - TTAAAGTAGAATCTGCGTCGGAGACGAAGTCATTAAGATCTGAATCGACAAGTAGTGTGC - 8880
   -LK * NLRRRRSH * DLNRQVVC
       SRICVGDEVIKI*IDK*CA
      K V E S A S E T K S L R S E S T S S V P
8881 - CAGTTGGCAACCATTGTCTGAGCACAGCTGTACCTGGTGCAACTCCTTTATCAGAGCCAG - 8940
   -QLATIV * AQLYLVQLLYQSQ
    S W Q P L S E H S C T W C N S F I R A S
      V G N H C L S T A V P G A T P L S E P A
- H Q S E * L S C C R V Q L K * V Y L S I
    T K V N N S H V V G Y S * S K C I * V L
     PK * I T L M L * G T A K V S V F K Y *
9001 - GACACAGTTGAGTATACTTTGCGACATTCATCATTATTCCTTTTGGTATAACAGCATTTT - 9060
   -DTVEYTLRHSSLFLLV*QHF
    T Q L S I L C D I H H Y S F W Y N S I F
      H S * V Y F A T F I I I P F G I T A F S
9061 - CACCATAATTCTGAAGGTCACACTTTTCAAGAAGCATTCTTTGCATCTTGTACAAGTTAG - 9120
   - H H N S E G H T F Q E A F F A S C T S *
    TIILKVTLFKKHSLHLVQVR
      P * F * R S H F S R S I L C I L Y K L G
9121 - GCATCGCAACACCTGGTTGCCACGCTTGACTTGTTGTTTTTGGGTAGAAGGTTTCAA - 9180
   - A S Q H L V A T L D L L V V L G R R F Q
    HRNTWLPRLTCL*FWVEGFN
     I A T P G C H A * L A C S F G * K V S T
9181 - CATGTCCATCCTTACACCAAAGCATGAATGAAATTTCAGCATAGTCAATTGTAACCTTGA - 9240
   - H V H P Y T K A * M K F Q H S Q L * P *
    MSILTPKHE * NFSIVNCNLD
      C P S L H Q S M N E I S A * S I V T L T
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9241 - CCACTTTTGAAATCACTGACAAATCTTGTGACTTATTATCTCGACAAAGTCATCAAGTA - 9300
   - P L L K S L T N L V T L L S R Q S H Q V
     HF*NH*QIL*LYYLDKVIK*
      T F E I T D K S C D F I I S T K S S S K
9301 - AAAGATCAATCACAGAACACACATTTTGATGAACCTGTTTTGCGCATCTGTTATGAAGT - 9360
   -KDQSQNTHILMNLFAHLL*S
   - KINHRTHTF * * TCLRICYEV
      R S I T E H T H F D E P V C A S V M K *
9361 - AATTTTTCACTGTGCTGTCCATAGGGATAAAATCCTCTAATTTAAGTGGTGAATCTTGTG - 9420
   - N F S L C C P * G * N P L I * V V N L V
     IFHCAVHRDKIL*FKW*IL*
      F F T V L S I G I K S S N L S G E S C E
9421 - AGCGCTTGGCTAAGCCTATCATTAAATGAAGACCGCCAAGTTGTCCATGACTGAAATCTC - 9480
   -SAWLSLSLNEDRQVVHD*NL
    ALG * AYH * MKTAKLS MTEIS
      R L A K P I I K * R P P S C P * L K S P
9481 - CATAAACGATGTGTTCGAAGGCATAGCCCTCGAGCTTATATCGCTGTATGAATTCATCCA - 9540
   INDVFEGIALELISLYEFIH
     * T M C S K A * P S S L Y R C M N S S I
9541 - TAGCGAGCTCGAGAAAGTCAGTTTCCATTTGTGATCTGGGCTTAAAATCCTCTAAGTCTC - 9600
   - * R A R E S Q F P F V I W A * N P L S L
     SELEKVSFHL*SGLKIL*VS
     ASSRKS V S I C D L G L K S S K S L
9601 - TGCTCTGAGTAAAGTAGGTTTCAGGCAACTGTTGAATAATGCCGTCTACTTTCTTAAAGT - 9660
   ALSKVGFRQLLNNAVYFLKV
     L * V K * V S G N C * I M P S T F L K *
9661 - AGTTAAACTGTGTTTTTACTGATTCTCCAATTAATGTGACTCCATTGACGCTAGCTTGTG - 9720
   -S * T V F L L I L Q L M * L H * R * L V
     V K L C F Y * F S N * C D S I D A S L C
      LNCVFTDSPINVTPLTLACA
9721 - CTGGTCCCTTTGAAGGTGTTAGACCTTTGACTGAACCTTCTGTTATTAAAACACCATTAC - 9780
   - L V P L K V L D L * L N L L L K H H Y
     WSL*RC*TFD*TFCY*NTIT
      G P F E G V R P L T E P S V I K T P L R
9781 - GGGCGTTTCTAAAAAGGTCTACCTGTCCTTCCACTCTACCATCAAACAAGACAGTAAGTG - 9840
    -GRF * KGLPVLPLYHQTRQ * V
     G V S K K V Y L S F H S T I K Q D S K *
      A F L K R S T C P S T L P S N K T V S E
-KNKHSQ * VSWQCQSLCRHLL
     R T S T L S R F L G N V S H C A D T Y C
     E Q A L S V G F L A M S V I V Q T P I V
9901 - TAGATACATGTGCTGGGGCTTCTCTTTTGTAGTCCCAGATTACAGTATTAGCAGCGATAT - 9960
    - * I H V L G L L F C S P R L Q Y * Q R Y
     RYMCWGFSFVVPDYSISSDI
      D T C A G A S L L * S Q I T V L A A I S
9961 - CAACACCCAAATTATTGAGTATCTTAATCTCTGGCACTGGTTTAATGTTACGCTTAGCCC - 10020
    NTQIIEYLNLWHWFNVTLSP
      T P K L L S I L I S G T G L M L R L A Q
10021 - AAAGCTCAAATGCAACATTAACAGGAAGTGTTGTCTTATTTTCAAAGATCTCCACATCAA - 10080
    -KAQMQH*QEVLSYFQRSPHQ
     K L K C N I N R K C C L I F K D L H I N
       S N A T L T G S V V L F S K I S T S I
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10081 - TACCATCTACCTTTGTGTAAACAGCATTATTAATGATGGAAACAGGTGCTTCGCCGGCGT - 10140
    - Y H L P L C K Q H Y * * W K Q V L R R R
    - TIYLC V N S I I N D G N R C F A G V
      PSTFV*TALLMMETGASPAC
10141 - GTCCATCAAAGTGTCCTTTATTAACAACATTATAAGCCACATTTTCTAAACTCTGTAACC - 10200
    -V H Q S V L Y * Q H Y K P H F L N S V T
    - S I K V S F I N N I I S H I F * T L * P
      PSKCPLLTTL * ATFSKLCNL
-W * M Y S T G Y K Y Q I V C K S I G * I
    - G K C I P Q V I S I K L F V N P * A K S
      V N V F H R L * V S N C L * I H R L N P
10261 - CAGCAGAAATCATCATATTATATGCATCCAAGTACTGTCGGTACTCATTTGCATGGTGTC - 10320
    - O O K S S Y Y M H P S T V G T H L H G V
    - S R N H H I I C I Q V L S V L I C M V S
       A E I I I L Y A S K Y C R Y S F A W C L
10321 - TGCAAACAGCACCACCTAAATTGCATCGTGTAATACACGTAGCAGATTTGAGTGGAACAT - 10380
    - C K Q H H L N C I V * Y T * Q I * V E H
    - ANSTT * IASCNTRS RFE W N I
       Q T A P P K L H R V I H V A D L S G T *
10381 - AATCAATATCCGACACTACTTGTTTGCCATGAGACTCACAAGGACTATCAGAATAGTAAA - 10440
    -NQYPTLLVCHETHKDYQNSK
    - INIRHYLFAMRLTRIVK
       SISDTTCLP*DSQGLSE**K
10441 - AGAAAGGCAATTGCTTTAAATTAGTAAATGCACTTTTATCGAAAGCTGGAGTGTGGAATG - 10500
    -R K A I A L N * * M H F Y R K L E C G M
    - E R Q L L * I S K C T F I E S W S V E C
       K G N C F K L V N A L L S K A G V W N A
10501 - CATGCTTATTCACATACAAACTACCACCATCACAGCCTGGTAAGTTCAAGTTTGACAAGA - 10560
    - H A Y S H T N Y H H H S L V S S S L T R
    - M L I H I Q T T T I T A W * V Q V * Q D
       CLFTYKLPPSQPGKFKFDKT
10561 - CTCTTGTGTCAAACCTACACACACTTGCATTGGCTGGGTAACGATCAACGTTACAATTCC - 10620
    -L L C Q T Y T Q L H W L G N D Q R Y N S
    - S C V K P T H N C I G W V T I N V T I P
      L V S N L H T I A L A G * R S T L Q F Q
10621 - AAAACAAACAACACCATCAGTGAATTTATCGTGATGTGTAGCATAAGAATAGAAGAGTT - 10680
    -KTNKHHQ*IYRDV*HKNRRV
    - K Q T N T I S E F I V M C S I R I E E F
      N K Q T P S V N L S * C V A * E * K S S
10681 - CCTCTATTTTGTAAGCTTTGTCACTACATGGCTGAGCATCGTAGAACTTCCATTCTACTT - 10740
    -PLFCKLCHYMAEHRRTSILL
    - L Y F V S F V T T W L S I V E L P F Y F - S I L * A L S L H G * A S * N F H S T S
10741 - CAGCCTGAGGCACACTTGATAGCCTTTGGATTTCCAATGTCATGAAGAACTGGAAACT - 10800
    -QPEAHT * * PLDFQCHEELET
     S L R H T L D S L W I S N V M K N W K L
     A * G T H L I A F G F P M S * R T G N L
10801 - TATCAGCAAGCAATGCAGACTTCACAACCATGTGTTGTTACTTTTCTGCAAGCAGAATTAA - 10860
    -YQQAMQTSQPCVVLFCKQN*
     I S K Q C R L H N H V L Y F S A S R I N
      S A S N A D F T T M C C T F L Q A E L T
10861 - CCCTCAGTTCATCTCCTATAATAGGGTATTCAACAGACCAATCAACGCGCTTAACAAAGC - 10920
    -PSVHLL**GIQQTNQRA*QS
     P Q F I S Y N R V F N R P I N A L N K A
      LSSSPIIGYSTDQSTRLTKH
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10921 - ACTCATGGACTGCTAAACATCTAGTCATGATAGCATCACAACTAGCCACATGTGCATTTC - 10980
    – L M D C \star T S S H D S I T T S H M C I S
       S W T A K H L V M I A S Q L A T C A F P
10981 - CATGTACCTGGCAATGTTGGTCATGGTTACTCTGAAGGTTACCCGTAAAGCCCCACTGCT - 11040
    - H V P G N V G H G Y S E G Y P * S P T A
    \hbox{-} \quad \hbox{M} \quad \hbox{Y} \quad \hbox{L} \quad \hbox{A} \quad \hbox{M} \quad \hbox{L} \quad \hbox{V} \quad \hbox{M} \quad \hbox{V} \quad \hbox{T} \quad \hbox{L} \quad \hbox{K} \quad \hbox{V} \quad \hbox{T} \quad \hbox{R} \quad \hbox{K} \quad \hbox{A} \quad \hbox{P} \quad \hbox{L} \quad \hbox{L}
       CTWQCWSWLL*RLPVKPHC*
11041 - GAACATCAATCATAAATGGGTTATAGACATAGTCAAAACCCACAGAATGATTCCAGCAGG - 11100
    -E H Q S * M G Y R H S Q N P Q N D S S R
      N I N H K W V I D I V K T H R M I P A G
       TSIINGL*T*SKPTE*FQQA
11101 - CATAAGTATCTGATGAAGTAGAAAAGCAAGTTGCACGTTTGTCACACAGACAACACGTTC - 11160
    - H K Y L M K * K S K L H V C H T D N T F
    - I S I * * S R K A S C T F V T Q T T R S
       * V S D E V E K Q V A R L S H R Q H V L
11161 - TTTCAGGTCCAATCTTGACAAAGTACTTCATTGATGTAAGCTCAAAGCCATGCGCCCAAA - 11220
    - F Q V Q S * Q S T S L M * A Q S H A P K
    - F R S N L D K V L H * C K L K A M R P K
       S G P I L T K Y F I D V S S K P C A Q R
11221 - GGACGAACACGACTCTGTCTGACAATCCTTTCAGTGTATCACTGAGCATTTGTACTATCT - 11280
    -GRTRLCLTILSVYH*AFVLS
    - D E H D S V * Q S F Q C I T E H L Y Y L
       T N T T L S D N P F S V S L S I C T I L
11281 - TAATACGCACTACATTCCAGGGCAAGCCTTTATACATGAGTGGTATAAGATGTTTAAACT - 11340
    - * Y A L H S R A S L Y T * V V * D V * T
    - N T H Y I P G Q A F I H E W Y K M F K L
       IRTTFOGKPLYMSGIRCLNW
11341 - GGTCACCTGGTGGAGGTTTTGCATTAACTCTGGTGAATTCTGTGTTATTTTCAGTGTCAA - 11400
    -G H L V E V L H * L W * I L C Y F Q C Q
    - V T W W R F C I N S G E F C V I F S V N
       S P G G F A L T L V N S V L F S V S T
11401 - CATAACCAGTCGGTACAGCTACTAAGTTAACACCTGTAGAAAATCCTAGCTGGAGAGGTA - 11460
    - H N Q S V Q L L S * H L * K I L A G E V
     ITSRYSY*VNTCRKS*LER*
      .* P V G T A T K L T P V E N P S W R G R
11461 - GGTTAGTACCCACAGCATCTCTAGTTGCATGACAGCCCTCTACATCAAAGCCAATCCACG - 11520
    -G * Y P Q H L * L H D S P L H Q S Q S T
     V S T H S I S S C M T A L Y I K A N P R
       L V P T A S L V A * Q P S T S K P I H A
11521 - CACGAACGTGACGAATAGCTTCTTCGCGGGTGATAAACATATTAGGGTAACCATTGACTT - 11580
    - H E R D E * L L R G * * T Y * G N H * L
     TNVTNSFFAGDKHIRVTIDL
       R T * R I A S S R V I N I L G * P L T W
11581 - GGTAATTCATTTTGAAACCCATCATAGAGATGAGTCTACGGTAGGTCATGTCCTTTGGTA - 11640
    -GNSF*NPS*R*VYGRSCPLV
      V I H F E T H H R D E S T V G H V L W Y
       * FILKPIEMSLR * VMSFGM
11641 - TGCCTGGTATGTCAACACATAATCCTTCAGTCTTGAATTTTATATCAACGCTGAGGTGTG - 11700
     -CLVCQHIILQS*ILYQR*GV
      AWYVNT * SFSLEFYIN A E V C
      P G M S T H N P S V L N F I S T L R C V
11701 - TAGGTGCCTGTGTAGGATGAAGACCAGTAATGATCTTACTACAGTCCTTAAAAAGTCCAG - 11760
    - * V P V * D E D Q * * S Y Y S P * K V Q
    - R C L C R M K T S N D L T T V L K K S S
      GACVG * RPVMILLQSLKSPV
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11761 - TTACATTTTCTGCTTGTAATGTAGCCACATTGCGACGTGGTATTTCTAGACTTGTAAATT - 11820
     -LHFLLVM*PHCDVVFLDL*I
     - Y I F C L * C S H I A T W Y F * T C K L
        T F S A C N V A T L R R G I S R L V N C
11821 - GCAGTTTGTCATAAAGATCTCTATCAGACATTATGCACAAAATGCCAATTTTTGCCCTTG - 11880
     - A V C H K D L Y Q T L C T K C Q F L P L
        \begin{smallmatrix} Q \end{smallmatrix}  \  \, F \hspace{.1cm} V \hspace{.1cm} I \hspace{.1cm} K \hspace{.1cm} I \hspace{.1cm} S \hspace{.1cm} I \hspace{.1cm} R \hspace{.1cm} H \hspace{.1cm} Y \hspace{.1cm} A \hspace{.1cm} Q \hspace{.1cm} N \hspace{.1cm} A \hspace{.1cm} N \hspace{.1cm} F \hspace{.1cm} C \hspace{.1cm} P \hspace{.1cm} C \\
        S L S * R S L S D I M H K M P I F A L V
11881 - TGATAGCCACATTGAAGCGGTTGACATTACAAGAGTGTGCTGTTTCAGTAGTTTGTGTGA - 11940
     - * * P H * S G * H Y K S V L F Q * F V *
     - D S H I E A V D I T R V C C F S S L C E
        I A T L K R L T L Q E C A V S V V C V N
11941 - ATATGACATAGTCATATTCAGAACCCTGTGATGAATCAACAGTCTGCGTAGGCAATCCTA - 12000
     -I * H S H I Q N P V M N Q Q S A * A I L
     - Y D I V I F R T L * * I N S L R R Q S *
        M T * S Y S E P C D E S T V C V G N P K
12001 - AGATTTTTGAAGCTACAGCGTTCTGTGAATTATAAGGTGAGATAAAAAACAGCTTTTCTCC - 12060
     - R F L K L Q R S V N Y K V R * K Q L F S - D F * S Y S V L * I I R * D K N S F S P
        I F E A T A F C E L * G E I K T A F L Q
12061 - AAGCAGGATTGCGTGTAAGAAATTCTCTTACAACGCCTATTTGAGGTCTGTTGATTGCAG - 12120
     -KQDCV*EILLQRLFEVC*LQ
     - S R I A C K K F S Y N A Y L R S V D C R
        AGLRVRNSLTTPI*GLLIAD
12121 - ATGAAACATCATGTGTAATAACACCTTTGTAGAACATTTTGAAGCATTGAGCTGACTTAT - 12180
     - M K H H V * * H L C R T F * S I E L T Y
     - * N I M C N N T F V E H F E A L S * L I
        ETSCVITPL*NILKH*ADLS
12181 - CCTTGTGTGCTTTTTAGCTTATTGTCATAAACTAAAGCACTCACAGTGTCAACAATTTCAG - 12240
     - P C V L L A Y C H K L K H S Q C Q Q F Q
     - L V C F * L I V I N * S T H S V N N F S
        LCAFSLLS * TKALTVSTISA
12241 - CAGGACAACGGCGACAAGTTCCAAGGAACATGTCTGGACCTATTGTTTTCATAAGTCTGC - 12300
     -Q D N G D K F Q G T C L D L L F S * V C
     - R T T A T S S K E H V W T Y C F H K S A
        G Q R R Q V P R N M S G P I V F I S L H
12301 - ACACTGAATTAAAATATTCTGGTTCTAGTGTGCCTTTAGTCAGCAATGTGCGGGGGGCTG - 12360
     - T L N * N I L V L V C L * S A M C G G L - H * I K I F W F * C A F S Q Q C A G G W
        TELKYSGSSVPLVSNVRGAG
12361 - GTAATTGAGCAGGATCGCCAATATAGACGTAGTGTTTTGCACGAAGTCTAGCATTGACAA - 12420
     -VIEQDRQYRRSVLHEV*H*Q
       * L S R I A N I D V V F C T K S S I D N
        N * A G S P I * T * C F A R S L A L T T
12421 - CACTCAAGTCATAATTAGTAGCCATAGAGATTTCATCAAAGACTACAATGTCAGCAGTTG - 12480
     - H S S H N * * P * R F H Q R L Q C Q Q L
     - T Q V I I S S H R D F I K D Y N V S S C
       LKS * L V A I E I S S K T T M S A V V
12481 - TTTCTGGCAATGCATTTACAGTGCAGAAAACATACTGTTCTAGTGTTGAATTCACTTTGA - 12540
     -FLAMHLQCRKHTVLVLNSL*
      FWQCIYSAENILF*C*IHFE
        SGNAFTVQKTYCSSVEFTLN
12541 - ATTTATCAAAACACTCTACGCGCGCACGCGCAGGTATGATTCTACTACATTTATCTATGG - 12600
     -IYQNTLRAHAQV*FYYIYLW
     - FIKTLYARTRRYDSTTFIYG
       LSKHSTRARAGMILLHLSMG
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12601 - GCAAATATTTTAATGCCTTTTCACATAGGGCATCAACAGCTGCATGAGAGCATGCCGTAT - 12660
     -ANILMPFHIGHQQLHESMPY
     - Q I F * C L F T * G I N S C M R A C R I
        KYFNAFSHRASTAA*EHAVY
12661 - ACACTATGCGAGCAGATGGGTAATAGAGAGCAAGTCCGATGGCAAAATGACTCTTACCAG - 12720
     -TLCEQMGNREQVRWQNDSYQ
     - H Y A S R W V I E S K S D G K M T L T S
         \texttt{T} \ \texttt{M} \ \texttt{R} \ \texttt{A} \ \texttt{D} \ \texttt{G} \ \star \ \star \ \texttt{R} \ \texttt{A} \ \texttt{S} \ \texttt{P} \ \texttt{M} \ \texttt{A} \ \texttt{K} \ \star \ \texttt{L} \ \texttt{L} \ \texttt{P} \ \texttt{V} 
12721 - TACCAGGTGGTCCTTGGAGTGTAGAGTACTTTTGCATGCCGACCTTTTGATAATTTGCAA - 12780
     -YQVVLGV*STFACRPFDNLQ
     - T R W S L E C R V L L H A D L L I I C N
        P G G P W S V E Y F C M P T F * * F A T
12781 - CATTGCTAGAAAACTCATCTGAGATGTTGAGTGTTGGGTACAAGCCAGTAATTCTCACAT - 12840
     - H C * K T H L R C * V L G T S Q * F S H
     - I A R K L I * D V E C W V Q A S N S H I
       LLENSSEMLSVGYKPVILT
12841 - AGTGCTCTTGTGGCACTAGAGTAGGTGCACTAAGTGGCATTACAGTGTGAGATGTCAACA - 12900
     -SALVALE * V H * V A L Q C E M S T
     - V L L W H * S R C T K W H Y S V R C Q H
        C S C G T R V G A L S G I T V * D V N T
12901 - CAAAGTAATCACCAACATTCAACTTGTATGTCGTAGTACCTCTGTACACAACAGCATCAC - 12960
     -QSNHQHSTCMS*YLCTQQHH
     - K V I T N I Q L V C R S T S V H N S I T
        K * S P T F N L Y V V P L Y T T A S P
12961 - CATAGTCACCTTTTTCAAAGGTGTACTCTCCAATCTGTACTTTACTATTTTTAGTTACAC - 13020
     -HSHLFQRCTLQSVLYYF*LH
     - I V T F F K G V L S N L Y F T I F S Y T
        * S P F S K V Y S P I C T L L F L V T R
13021 - GGTAACCAGTAAAGACATAGTTTCTGTTCAATGGTGGTCTAGGTTTTCCAACCTCCCATG - 13080
     -GNQ * RHS FC SM V V * V FQ P P M
     - V T S K D I V S V Q W W S R F S N L P *
        * P V K T * F L F N G G L G F P T S H E
13081 - AAAGATGCAATTCTCTGTCAGAGAGTACTTCGCGTACAGTGGCAATACCATATGACAGCT - 13140
     -KDAILCQRVLRVQWQYHMTA
     - K M Q F S V R E Y F A Y S G N T I * Q L
        RCNSLSESTSRTVAIPYDSL
13141 - TAAATGTTTCCTCAGTGGCTTTGAGCGTTTCTGCTGCGAAAAGCTTGAGTCTCTCAGTAC - 13200
     - * M F P Q W L * A F L L R K A * V S Q Y
     - K C F L S G F E R F C C E K L E S L S T
        N V S S V A L S V S A A K S L S L S V Q
13201 - AAGTGTTGGCAAGTATGTAATCGCCAGCATTAGTCCAATCACATGTTGCTATCGCATTGA + 13260
     -KCWQVCNRQH * SNHMLLSH *
     - S V G K Y V I A S I S P I T C C Y R I E
        V L A S M * S P A L V Q S H V A I A L K
13261 - AGTCAGTGACATTGTCACTGCCTACACATGTGTTTTTGTATAAACCAAAAACCTGACCAT - 13320
     -SQ * H C H C L H M C F C I N Q K P D H
     - V S D I V T A Y T C V F V * T K N L T I
        S V T L S L P T H V F L Y K P K T * P L
13321 - TAGCACATAATGGAAAACTAATGGGAGGCTTATGTGACTTGCAATAATAGCTCATACCTC - 13380
     - * H I M E N * W E A Y V T C N N S S Y L
     - S T * W K T N G R L M * L A I I A H T S
        A H N G K L M G G L C D L Q * * L I P P
13381 - CTAGATACAGTTGTCACATCAGTGACATCACAACCTGGGGCATTGCAAACATAGGGAT - 13440
     -L D T V V S H Q * H H N L G H C K H R D
       * I Q L C H I S D I T T W G I A N I G I
        R Y S C V T S V T S Q P G A L Q T * G L
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13441 - TAACAGACAACATAATTTGTGTGATGTTGAAATGACATGGTCATAGCAGCACTTGCAAC - 13500
    - * Q T T L I C V M L K * H G H S S T C N
    - N R Q H * F V * C * N D M V I A A L A T
       T D N T N L C D V E M T W S * Q H L Q H
13501 - ATAGGAATGGTCTCCTAATACAGGCACCGCAACGAAGTGAAGTCTGTGAATTGCACAATA - 13560
    - I G M V S * Y R H R N E V K S V N C T I
    - * E W S P N T G T A T K * S L * I A Q Y
       RNGLLIQAPQRSEVCELHNT
13561 - CACAAGCACCTACAGCCTGCAAGACTGTATGTGGTGTGTACATAGCCTCATAAAACTCAG - 13620
    - H K H L Q P A R L Y V V C T * P H K T Q
    - T S T Y S L Q D C M W C V H S L I K L R
       Q A P T A C K T V C G V Y I A S * N S G
13621 - GTTCCCAGTACCGTGAGGTGTTATCATTAGTTAGCATTACGGAATACATGTCCAACATGT - 13680
    -V P S T V R C Y H * L A L R N T C P T C
    - F P V P * G V I I S * H Y G I H V Q H V
      S Q Y R E V L S L V S I T E Y M S N M W
13681 - GGCCAGTAAGCTCATCATGTAACTTTCTAATGTATTGTAAATACAAGTGAAAGACATCAG - 13740
    -GQ * A H H V T F * C I V N T S E R H Q
    - A S K L I M * L S N V L * I Q V K D I S
       P V S S S C N F L M Y C K Y K * K T S A
13741 - CATACTCCTGATTAGGATGTTTTGTAAGTGGGTAAGCATCAATAGCCAGTGACACGAACC - 13800
    - H T P D * D V L * V G K H Q * P V T R T
    - I L L I R M F C K W V S I N S Q * H E P
      YS*LGCFVSG*ASIASDTNL
13801 - TTTCAATCATAAGTGTACCATCTGTTTTGACAATATCATCGACAAAACAGCCTGCGCCTA - 13860
    -FQS*VYHLF*QYHRQNSLRL
    - FNHKCTICFDNIIDKTACA*
      SIISVPSVLTISSTKQPAPN
13861 - ATATTCTTGATGGATCTGGGTAAGGCAGGTACACGTAATCATCTCCTTGTTTAACTAGCA - 13920
    -IFLM D L G K A G T R N H L L V * L A
    - Y S * W I W V R Q V H V I I S L F N * H
       I L D G S G * G R Y T * S S P C L T S I
13921 - TTGTATGCTGTGAGCAAAATTCGTGAGGTCCTTTAGTAAGGTCAGTCTCAGTCCAACATT - 13980
    -LYAVSKIREVL**GQSQSNI
    - C M L * A K F V R S F S K V S L S P T F
      V C C E Q N S * G P L V R S V S V Q H F
13981 - TTGCCTCAGACATGAACACATTATTTTGATAATAAAGAACTGCCTTAAAGTTCTTAATGC - 14040
    -LPQT * THYFDNKELP * SS * C
    - C L R H E H I I L I I K N C L K V L N A - A S D M N T L F * * * R T A L K F L M L
14041 - TAGCTACTAAACCTTGAGCCGCATAGTTACTGTTATAGCACACACGGCATCATCAGAAA - 14100
    - * L L N L E P H S Y C Y S T Q R H H Q K
    - S Y * T L S R I V T V I A H N G I I R K
      ATKP*AA*LLL*HTTASSER
14101 - GAATCATCATGGAGAAATGTTTACGCAGGTAAGCGTAAAACTCATCCACGAATTCATGAT - 14160
    -ESSWRNVYAGKRKTHPRIHD
    - N H H G E M F T Q V S V K L I H E F M I
- I I M E K C L R R * A * N S S T N S * S
14161 - CAACATCCCTATTTCTATAGAGACACTCATAGAGCCTGTGTTGTAGATTGCGGACATACT - 14220
    -Q H P Y F Y R D T H R A C V V D C G H T
    - N I P I S I E T L I E P V L * I A D I L - T S L F L * R H S * S L C C R L R T Y L
14221 - TGTCAGCTATCTTATTACCATCAGTTGAAAGAAGTGCATTTACATTGGCTGTAACAGCTT - 14280
    -CQLSYYHQLKEVHLHWL*QL
     V S Y L I T I S * K K C I Y I G C N S L
       SAILLPSVERSAFTLAVTA*
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14281 - GACAAATGTTAAAGACACTATTAGCATAAGCAGTTGTAGCATCACCGGATGATGTTCCAC - 14340
    - D K C * R H Y * H K Q L * H H R M M F H
      T N V K D T I S I S S C S I T G * C S T
       Q M L K T L L A * A V V A S P D D V P P
14341 - CTGGTTTAACATATAGTGAGCCGCCACACATGACCATCTCACTTAATACTTGCGCACACT ~ 14400
    -LV * HIVSRHT * PSHLILAHT
    - W F N I * * A A T H D H L T * Y L R T L
       G L T Y S E P P H M T I S L N T C A H S
14401 - CGTTAGCTAACCTGTAGAAACGGTGTGATAAGTTACAGCAAGTGTTATGTTTGCGAGCAA - 14460
    -R * L T C R N G V I S Y S K C Y V C E Q
    - V S * P V E T V * * V T A S V M F A S K
       LANL * KRCDKLQQVLCLRAR
14461 - GAACAAGAGAGGCCATTATCCTAAGCATGTTAGGCATGGCTCTGTCACATTTTGGATAAT - 14520
    -EQERPLS * A C * A W L C H I L D N
    - N K R G H Y P K H V R H G S V T F W I I
       TREAILS MLG MALS HFG * S
14521 - CCCAACCCATAAGGTGTGGAGTTTCTACATCACTGTAAACAGTTTTTAACATATTATGCC - 14580
    -PNP*GVEFLHHCKQFLTYYA
    - P T H K V W S F Y I T V N S F * H I M P
       Q P I R C G V S T S L * T V F N I L C Q
14581 - AGCCACCGTAAAACTTGCTTGTTCCAATTACCACAGTAGCTCCTCTAGTGGCGGCTATTG - 14640
    -SHRKTCLFQLPQ*LL*WRLL
    - A T V K L A C S N Y H S S S S G G Y *
       PP * N L L V P I T T V A P L V A A I D
14641 - ACTTCAATAATTTCTGATGAAACTGTCTATTTGTCATAGTACTACAGATAGAGACACCAG - 14700
    -TSIISDETVYLS*YYR*RHQ
    - L Q * F L M K L S I C H S T T D R D T S
      FNNF * * NCLFVIVLQIETPA
14701 - CTACGGTGCGAGCTCTATTCTTTGCACTAATGGCATACTTAAGATTCATTTGAGTTATAG - 14760
    -LRCELYSLH * WHT * DSFEL *
    - Y G A S S I L C T N G I L K I H L S Y S
      T V R A L F F A L M A Y L R F I * V I V
14761 - TAGGGATGACATTACGCTTAGTATACGCGAAAAGTGCATCTTGATCCTCATAACTCATTG - 14820
    - * G * H Y A * Y T R K V H L D P H N S L
    - R D D I T L S I R E K C I L I L I T H *
- G M T L R L V Y A K S A S * S S * L I E
14821 - AGTCATAATAAAGTCTAGCCTTACCCCATTTATTAAATGGGAAACCAGCTGATTTATCCA - 14880
    -SHNKV*PYPIY*MGNQLIYP
-VIIKSSLTPFIKWETS*FIQ
       S * * S L A L P H L L N G K P A D L S R
14881 - GATTGTTAACGATTACTTGGTTGGCATTAATACAGCCACCATCGTAACAATCAAAGTATT - 14940
    -DC * RLLGWH * YSHHRNNQSI
      I V N D Y L V G I N T A T I V T I K V F L L T I T W L A L I Q P P S * Q S K Y L
14941 - TATCAACAACTTCAACTACGAATAGGAGTTGTCTGATATCACACATTGTTGGCAGATTAT - 15000
    - Y Q Q L Q L R I G V V * Y H T L L A D Y
      INNFNYE*ELSDITHCWQII
       STTSTTNRSCLISHIVGRL*
15001 - AACGATAATAGTCATAATCACTGATAGCAGCGTTGCCATCCTGAGCAAAGAAGAAGTGTT - 15060
    -NDNSHNH**QRCHPEQRRSV
      TIIVIIT DSSVAILSKEEVF
       R * * S * S L I A A L P S * A K K C F
15061 - TTAGTTCAACAGAACTTCCTTCCTTAAAGAAACCTTTAGACACAGCAAAGTCATAAAAGT - 15120
    -LVQQNFLP*RNL*TQQSHKS
-*FNRTSFLKETFRHSKVIKV
       S S T E L P S L K K P L D T A K S * K S
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-LY*NYRV*QFEKQHCLLVQL
    - FIKITGFDSLKSNIVC * CSY
     LLKLPGLTV * KATLFVSAAT
-L K S M * C V Y L A I N C Q K L H A * L
     * K A C S A F I * Q * I A R S C M H S W
     EKHVVRLSSNKLPEAACIAG
15241 - GATCAGCAGCATACACTAAAAGTTCCTTGAAACTGAGACGCGAGCTATGTAAGTTTACAT - 15300
    -DQQHTLKVP*N*DASYVSLH
    - I S S I H * K F L E T E T R A M * V Y I
      S A A Y T K S S L K L R R E L C K F T S
15301 - CCTGATTATGTACGACTCCTAACTCACGAAAATGGTATCCAGTTGAAACAACAAAAGGAA - 15360
    -PDYVRLLTHENGIQLKQQKE
    - L I M Y D S * L T K M V S S * N N K R N
      * L C T T P N S R K W Y P V E T T K G T
15361 - CACCATCTACAAATATTTTCTTACTAGTGGTCCAAAACTTGTAGGTGGAAACACAGTAG - 15420
    - H H L Q I F F L L V V Q N L * V E T Q *
    - TIYKYFSY* WSKTCRWKHSR
      PSTNIFLTSGPKLVGGNTVE
15421 - AAAATAACACATTAAAGTTTGCACAATGAAGGATACACCTATCATCCAAACAGTTAATAC - 15480
    -KITH*SLHNEGYTYHPNS*Y
    - K * H I K V C T M K D T P I I Q T V N T
      N N T L K F A Q * R I H L S S K Q L I Q
15481 - AATTGGGATGGTATGTCTGGTCCCAATATTTAAAATAACGGTCGAAGAGACAAAGTCTCT - 15540
    -N W D G M S G P N I * N N G R R D K V S
    - I G M V C L V P I F K I T V E E T K S L
      L G W Y V W S Q Y L K * R S K R Q S L S
15541 - CTTCCGTAAAATCATATTTCAGCAAATCCCACTTAATAAGTGGTTTTGCGAGATCAGCAT - 15600
    -LP*NHISANPT**VVLRDQH
    - FRKIIFQQIPLNKWFCEISI
      S V K S Y F S K S H L I S G F A R S A S
15601 - CCATATGGGACTCAGCCAATGCCCTAGTCAAAGTGAGGATGGGCATCAGCAATGAGT - 15660
    -PYGTQQPMP*SK*GWASAMS
    - H M G L S S Q C P S Q S E D G H Q Q * V
      I W D S A A N A L V K V R M G I S N E *
15661 - AATATGAATCCACAATAGGAACTCCGCAGCCTGGTGCTACTTGTACGAAATCACCGAAAT - 15720
    -N M N P Q * E L R S L V L L V R N H R N
    - I * I H N R N S A A W C Y L Y E I T E I
      Y E S T I G T P Q P G A T C T K S P K S
15721 - CGTACCAGTTCCCATTAAGATCCTGATTATCTAATGTCAGTACGCCTACAATGCCTGCAT - 15780
    -RTSSH * DPDYLMSVRLQCLH
    - V P V P I K I L I I * C Q Y A Y N A C I
      Y O F P L R S * L S N V S T P T M P A S
15781 - CACGCATAGCATCGCAGAATTGTACAGTCTTTAATAATGATTGGCGTACACGCTCACCTA - 15840
    - H A * H R R I V Q S L I M I G V H A H L
- T H S I A E L Y S L * * * L A Y T L T *
      RIASQNCTVFNNDWRTRSPK
15841 - AGTTAGCATATACGCGTAAGATGTCAGGATTCTCTACGAAGTCATACCAATCCTTCTTAT - 15900
    -S * H I R V R C Q D S L R S H T N P S Y
    - V S I Y A * D V R I L Y E V I P I L L I
      LAYTRKMSGFSTKSYQSFLL
15901 - TGAAATAATCATCATCACAGCAATTGTATGTGACGAGTATTTCTTTTAATGTATCACAAT - 15960
    - * N N H H H S N C M * R V F L L M Y H N
    - E I I I I T A I V C D E Y F F * C I T I
      K * S S S O O L Y V T S I S F N V S Q L
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- Y P H Q N D V E H R L N Q P L C I * L D
    - T L I K M T * S I D * I S H C V F S * T
       PSSK*RRA*TKSAIVYLVRR
16021 - GCTGACGTGATATATGTGGTACCATGTCACCATCTAAACTTGAAAAAGTCATGGA - 16080
    - A D V I Y V V P C H H L L * T * K S H G
    - L T * Y M W Y H V T I Y S K L E K V M D
      * R D I C G T M S P S T L N L K K S W T
16081 - CAGCAACCGCTGGACAATCTTTAACCAAGTTATAAATAGTCTCTTCATGTTGGTAGTTAG - 16140
    -QQPLDNL*PSYK*SLHVGS*
      SNRWTIFNQVINSLFMLVVR
      A T A G Q S L T K L * I V S S C W * L D
16141 - ACATAGTATGCCTCTTAACTACAAAGTAAGAGTCTAATAAATTGCCTTCCTCATCCTTCT - 16200
    - T * Y A S * L Q S K S L I N C L P H P S
    - H S M P L N Y K V R V * * I A F L I L L
       I V C L L T T K * E S N K L P S S S F S
16201 - CCTGGAAGCGACAGCAATTAGTTTTTAGGAACTTTGCAAAACCAGCACTTTTTTCGTTGT - 16260
    - P G S D S N * F L G T L Q N Q H F F R C
    - L E A T A I S F * E L C K T S T F F V V
       W K R Q Q L V F R N F A K P A L F S L
16261 - AAATATCAAAAGCCCTGTAGACGACATCAGTACTAGTGCCTGTGCCGCACGGTGTAAGAC - 16320
    - K Y Q K P C R R H Q Y * C L C R T V * D
    - N I K S P V D D I S T S A C A A R C K T
       I S K A L * T T S V L V P V P H G V R R
16321 - GGGCTGCACTTACACCGCAAACCCGTTTAAAAACGTTGATGCATCCGCAGACTGCATCAA - 16380
    -GLHLHRKPV * KR * CIRRLHQ
    - G C T Y T A N P F K N V D A S A D C I K
       A A L T P Q T R L K T L M H P Q T A S R
16381 - GGGTTCGCGGAGTTGGTCACAACTACAGCCATAACCTTTCCACATTCCGCAGACGGTACA - 16440
    -GFAELVTTTAITFPHSADGT
    - G S R S W S Q L Q P * P F H I P Q T V Q
       V R G V G H N Y S H N L S T F R R Y R
- D C V S K C K T H W V I S T S G R Y L D
       \begin{smallmatrix} T & V & F & L & S & V & K & P & T & G & S & L & A & Q & V & G & I & W & T \\ \end{smallmatrix} 
       L C F * V * N P L G H * H K W * V F G R
16501 - GTACTTACCTTTCAAGTCACAGAATCCTTTAGGATTTGGATGGTCAATGTGGCATCTACA - 16560
    -V L T F Q V T E S F R I W M V N V A S T
     Y L P F K S Q N P L G F G W S M W H L Q
       TYLSSHRIL*DLDGQCGIYN
16561 - ATACAGACAACATGAAGCACCACCAAAGGACTCTTGGTCCATGTTAGCTTCTGGTGTTAC - 16620
    -IOTT * STTKGLLVHVSFWCY
    - Y R O H E A P P K D S W S M L A S G V T
       T D N M K H H Q R T L G P C * L L V L Q
16621 - AGTAATTGCCTGTCCTGTACCAGTGTGTGTACACAACATCTTCACACAGTTGGTGATTGG - 16680
    -SNCLSCTSVCTQHLHTVGDW
     VIACPVPVCVHNIFTQLVIG
       * L P V L Y Q C V Y T T S S H S W * L V
16681 - TTGTCCTCCACTTGCTAGGTAATCCTTATATGCTTTAGCAGGGTCTACTGCAAAAGCACA - 16740
    - L S S T C * V I L I C F S R V Y C K S T
- C P P L A R * S L Y A L A G S T A K A Q
- V L H L L G N P Y M L * Q G L L Q K H R
16741 - GAAGGAAAGCACAGTTGAATTGGCAGGTACTTCTGTAGCATTTCCAGCCTGAAGACGTAC - 16800
    -EGKHS*IGRYFCSISSLKTY
     KESTVELAGTSVAFPA*RRT
       R K A Q L N W Q V L L * H F Q P E D V L
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16801 - TGTAGCAGCTAAACTGCCCAGCACCATACCTCTATTTAGGTTGTTTAAGCCTTTGATGAA - 16860
    - C S S * T A Q H H T S I * V V * A F D E
- V A A K L P S T I P L F R L F K P L M K
- * Q L N C P A P Y L Y L G C L S L * * S
16861 - GTACAAGTATTTCACTTTAGGCCCTTTTGGTGTGTCTGTAACAAACCTACAAGGTGGTTC - 16920
    -V Q V F H F R P F W C V C N K P T R W F
    - Y K Y F T L G P F G V S V T N L Q G G S - T S I S L * A L L V C L * Q T Y K V V P
16921 - CAGTTCTGTGTAAATTGTACCTGTACCATCACTCTTAGGGAATCTAGCCCATTTGAGATC - 16980
    -Q F C V N C T C T I T L R E S S P F E I
      S S V * I V P V P S L L G N L A H L R S
       V L C K L Y L Y H H S * G I * P I * D L
16981 - TTGGTGGTCTGATAGTAATGCCAGCACAAACCTACCTCCCTTCGAATTGTTATAGTAGGC - 17040
    - W W S D S N A S T N L P P F E L L * * A
       G G L I V M P A Q T Y L P S N C Y S R Q
17041 - AAGTGCATTGTCATCAGTACAAGCTGTTTGTGTGGTACCAGCCGCACAGGACATCTGTCG - 17100
    -KCIVISTSCLCGTSRTGHLS
      S A L S S V Q A V C V V P A A Q D I C R
      V H C H Q Y K L F V W Y Q P H R T S V V
17101 - TAGTGCTACTGGACTCAGTTCATTATTCTGTAGTTTAACAGCTGAGTTGGCTCTTAGAGC - 17160
    - * C Y W T Q F I I L * F N S * V G S * S
    - S A T G L S S L F C S L T A E L A L R A
       V L L D S V H Y S V V * Q L S W L L E L
17161 - TGTAACAATAAGAGGCCAAGCCAAATTTGGTGAATTGTCCATGTTAATTTCACTAAGTTG - 17220
    -CNNKRPSQIW*IVHVNFTKL
    - V T I R G Q A K F G E L S M L I S L S *
       * Q * E A K P N L V N C P C * F H * V E
17221 - AACAATCTTGCTATCCGCATCAACAACTTGCTGGATTTCCCAGAGTGCAGATGCATATGT - 17280
    -NNLAIRINNLLDFPECRCIC
    - TILLSASTTCWISQSADAYV
       QSCYPHQQLAGFPRVQMHM*
17281 - AAAGGTGTTACCATCACAAGTGTTCTTGTAGGTACCATAATCAGGGACAACCATGAG - 17340
    -KGVTITSVLVGTIIRDNNHE
    - K V L P S Q V F L * V P * S G T T T M S
       RCYHHKCSCRYHNQGQP*V
17341 - TTTGGCTGCTGTAGTCAATGGTATGATGTTGAGTGGAACACAACCATCACGCGCATTGTT - 17400
    - F G C C S Q W Y D V E W N T T I T R I V
- L A A V V N G M M L S G T Q P S R A L L
      W L L * S M V * C * V E H N H H A H C *
17401 - GATAATGTTGTTAAGTGCATCATTATCAAGCTTCCTAAGCATAGTGAAGAGCATTGTTTG - 17460
    - D N V V K C I I I K L P K H S E E H C L
    - I M L L S A S L S S F L S I V K S I V C
       * C C * V H H Y O A S * A * * R A L F A
17461 - CATAGCACTAGTTACTTTTGCCCTCTTGTCCTCAGATCTTGCCTGTTTTGTACATTTGGGT - 17520
     - H S T S Y F C P L V L R S C L F V H L G
      I A L V T F A L L S S D L A C L Y I W V
       * H * L L P S C P Q I L P V C T F G S
- H S L I C H L F Q L A L H G S I T V K L
    - I A * S A I F S N L R C M A A S R S N S
       * P D L P S F P T C V A W Q H H G Q T Q
17581 - AGATTTAGCCACATTCAAAGATTTCTTTAACTTTTTGAGAACGACTTCAGAATCACCATT - 17640
     -RFSHIQRFL*LFENDFRITI
    - D L A T F K D F F N F L R T T S E S P L
         * P H S K I S L T F * E R L Q N H H *
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17641 - AGCTACAGCCTGCTCATAGGCCTCCTGGGCAGTGGCATAAGCGGCATATGATGGTAAAGA - 17700
    -SYSLLIGLLGSGISGI * W * R
    - A T A C S * A S W A V A * A A Y D G K E
       LQPAHRPPGQWHKRHMMVKN
17701 - ACTAAATTCTGAAGCAATAGCCTGAAGAGTAGCACGGTTATCGAGCATTTCCTCGCACAA - 17760
    -TKF*SNSLKSSTVIEHFLAQ
    - L N S E A I A * R V A R L S S I S S H N
       * I L K Q * P E E * H G Y R A F P R T T
17761 - CCTATTAATGTCTACAGCACCCTGCATGGATAGCAAAACAGACAAAAGAGAAAACCATCTT - 17820
    -PINVYSTLHG * QNRQKRNHL
    - L L M S T A P C M D S K T D K R E T I F
       Y * C L Q H P A W I A K Q T K E K P S S
17821 - CTCGAAAGCTTCAGTTGTGTCTTTTGCAAGAAGAATATCATTGTGGAGTTGTACACATTG - 17880
    -LESFSCVFCKKNIIVELYTL
    - S K A S V V S F A R R I S L W S C T H C
       RKLQLCLLQEEYHCGVVHIV
17881 - TGCCCACAATTTAGAAGATGACTCTACTCTAAGTTGTTGAAGAACCGAGAGCAGTACCAC - 17940
    -CPQFRR*LYSKLLKNREQYH
    - A H N L E D D S T L S C * R T E S S T T
       PTI * KMTLL * V V E E P R A V P Q
17941 - AGATGTGCACTTTACGTCAGACATTTTAGACTGTACAGTAGCAACCTTGATACATGGTTT - 18000
    -RCALYVRHFRLYSSNLDTWF
    - D V H F T S D I L D C T V A T L I H G L
       MCTLRQTF*TVQ*QP*YMVY
18001 - ACCTCCAATACCCAACAACTTAATGTTAAGCTTGAAAGCATCAATACTACTCTTAGGAGG - 18060
    -TSNTQQLNVKLESINTTLRR
    - PPIPNNLMLSLKASILLLGG
       L Q Y P T T * C * A * K H Q Y Y S * E A
18061 - CAAAAGCCCCTGGGAGTTCATATACCTAAATTCTTGTGTAGAGACCAAGTAGTCATAAAC - 18120
    -QKPLGVHIPKFLCRDQVVIN
    - K S P W E F I Y L N S C V E T K * S * T
       KAPGSSYT*ILV*RPSSHKH
18121 - ACCAAGAGTAAGCCTGAAGTAACGGTTGAGTAAACAGAAAAGGCCAAAGTAGCAGCAGCA - 18180
    - T K S K P E V T V E * T E K A K V A A A
     P R V S L K * R L S K Q K R P K * Q Q Q Q E * A * S N G * V N R K G Q S S S S N
18181 - ACAATAGCCTAAGAAACAATAAACAAGCATGATACACTGTAAGGTGTTGCCAGTAATAAA - 18240
    -TIA * ETINKH DTL * G V A S N K
    - Q * P K K Q * T S M I H C K V L P V I N
       N S L R N N K Q A * Y T V R C C Q * * I
18241 - TAACAATGGGTAATACTCAACACACACACACATATAGCTCTAGCTAAAAACATGATAGT - 18300
    - * Q W V I L N T H K H Y S S S * K H D S
    - N N G * Y S T H T N T I A L A K N M I V
       T M G N T Q H T Q T L * L * L K T * * S
18301 - CGTAACGACACCAGAATAGTTAGAGGTTACAGAAATAACTAAGGCCCACATGGAAATAGC - 18360
    -RNDTRIVRGYRNN*GPHGNS
     V T T P E * L E V T E I T K A H M E I A
       * R H Q N S * R L Q K * L R P T W K * L
18361 - TTGATCTAAAGCATTACCATAGTAGACTTTGTAAACAAGTGTAATGACATTCATCAGTGT - 18420
    - L I * S I T I V D F V N K C N D I H Q C
- * S K A L P * * T L * T S V M T F I S V
- D L K H Y H S R L C K Q V * * H S S V S
18421 - CCAAACACGTCTAGCAGCATCATCATAAACAGTGCGAGCTGTCATGAGAATAAGCAAAAC - 18480
    -PNTSSSIIINSASCHENKQN
      O T R L A A S S * T V R A V M R I S K T
       K H V * Q H H H K Q C E L S * E * A K L
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18481 - TAAAGCTGAAGCATACATAACACAATCCTTAAGCCTATAACCAGACAAGCTAGTGTCAGC - 18540
      S * S I H N T I L K P I T R Q A S V S
    - K A E A Y I T Q S L S L * P D K L V S A
      K L K H T * H N P * A Y N Q T S * C Q P
18541 - CAATTCAAGCCATGTCATGATACGCATCACCCAGCTAGCAGGCATGTAGACCATATTAAA - 18600
    -QFKPCHDTHHPASRHVDHIK
    - N S S H V M I R I T Q L A G M * T I L K
      I Q A M S * Y A S P S * Q A C R P Y * S
18601 - GTAAGCAACTGTTGCAAGAGAGGTAACAGAAACAAGCACAAGAATGCGTGCTTATGCTT - 18660
    - V S N C C K R R * Q K Q A Q E C V L M L
     * A T V A R E G N R N K H K N A C L C L
       K Q L L Q E K V T E T S T R M R A Y A *
18661 - AACAAGCAGCATAGCACATGCAGCAATTGCCATAATACCAAGAGTAAATGGCAAGAAAGC - 18720
    -N K Q H S T C S N C H N T K S K W Q E S
     T S S I A H A A I A I I P R V N G K K A
      Q A A * H M Q Q L P * Y Q E * M A R K H
18721 - ATTCTCGTAAACAAGAAAAACAGTGACCACTGTGTACTTTGAACAAGAATCAATAGTGA - 18780
    -I L V N K E K Q * P L C T L N K N Q * *
     FS*TKKNSDHCVL*TRINSD
       S R K Q R K T V T T V Y F E Q E S I V M
18781 - TGTCAAGAAAGTTAAAAGCATCCAATGATGAGTGCCCTTAACAATTTTCTTGAACTTACC - 18840
    -C Q E S * K H P M M S A L N N F L E L T
    - V K K V K S I Q * * V P L T I F L N L P
       S R K L K A S N D E C P * Q F S * T Y L
18841 - TTGGAAGGTAACACCAGAGCATTGTCTAACAACATCAAATGGTGTAAACTCATCTTCTAA - 18900
    -LEGNTRALSNNIKWCKLIF *
    - W K V T P E H C L T T S N G V N S S S K
       G R * H Q S I V * Q H Q M V * T H L L K
18901 - AATAGTGCTACCAAGGATAGTACGACCATTCATACCATTCTGCAGCAGCTCTTTCAAAGC - 18960
    -NSATKDSTTIHTILQQLFQS
      I V L P R I V R P F I P F C S S S F K A
      * C Y Q G * Y D H S Y H S A A A L S K Q
18961 - AGCACACATATCTAAGACGGCAATTCCTGTTTGAGCAGAAAGAGGTCCCAATATGTCAAC - 19020
    -STHI*DGNSCLSRKRSQYVN
    - A H I S K T A I P V * A E R G P N M S T
      H T Y L R R Q F L F E Q K E V P I C Q H
19021 - ATGATCTTGTGTCAAAGGTTCATAGTTGTACTTCATTGCCACAAGGTTAAAGTCATTCAA - 19080
    -MILCQRFIVVLHCHKVKVIQ
     * S C V K G S * L Y F I A T R L K S F K
       D L V S K V H S C T S L P Q G * S H S K
19081 - AGTAGTGGTGAATCTATTAAGAAACCACCTATCACCATTGATAACAGCAGCATACAGCCA - 19140
    -SSGESIKKPPITIDNSSIQP
    - V V V N L L R N H L S P L I T A A Y S H
      * W * I Y * E T T Y H H * * Q Q H T A M
-CQNI*CYGCVCTCSLCSLSV
     AKTFNVMVVSVPAACAVCLS
       P K H L M L W L C L Y L Q P V Q F V C Q
19201 - AACAAATGGACCATAGAATTTACCTTCTAAGTCAGTACCAGCGTGTACTCCTGTTGGAAG - 19260
    -N K W T I E F T F * V S T S V Y S C W K
      T N G P * N L P S K S V P A C T P V G S
       O M D H R I Y L L S Q Y Q R V L L E A
19261 - CTCCATATGATGCATATAGCAGAAAGACACGCAATCATAATCAATGTTAAAACCAACACT - 19320
    -LHMMHIAERHAIIINVKTNT
     SI * CI * Q K D T Q S * S M L K P T L
       P Y D A Y S R K T R N H N Q C * N Q H Y
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19321 - ACCACATGATCCATTAAGGAAAGAACCTTTAATGGTATGATTAGGTCTCATGGCACACTG - 19380
    -TT * S I K E R T F N G M I R S H G T L
    HMIH*GKNL*WYD*VSWHTD
19381 - ATAAACACCAGATGGTGAACCATTGTAGCATGCTAGAACTGAAAATGTTTGACCAGGTTG - 19440
   - I N T R W * T I V A C * N * K C L T R L
      TPDGEPL*HARTENV*PGW
      K H Q M V N H C S M L E L K M F D Q V G
19441 - GATACGGACAAATTTATACTTGGGTGTCTTAGGGTTAGAAGTATCAACTTTAAGCCTAAG - 19500
    -D T D K F I L G C L R V R S I N F K P K
     I R T N L Y L G V L G L E V S T L S L S
     Y G Q I Y T W V S * G * K Y Q L * A * A
19501 - CAGACAATTTTGCATAGAATGGCCAATAACACGAAGTTGAACATTGCCAGCCTGAACAAG - 19560
    -QTILHRMANNTKLNIASLNK
     R Q F C I E W P I T R S * T L P A * T R
      D N F A * N G Q * H E V E H C Q P E Q E
19561 - AAAGCTATGGTTGGATTTGCGAATGAGCAGATCTTCATAGTTAGGATTAAGCATGTCTTC - 19620
    -KAMVGFANEQIFIVRIKHVF
    - K L W L D L R M S R S S * L G L S M S S
     SYGWICE * ADLHS * D * ACLL
19621 - TGCTGTGCAAATGACATGTCTTGGACAGTATACTGTGTCATCCAACCACAATCCATTAAG - 19680
    -C C A N D M S W T V Y C V I Q P Q S I K
    - A V Q M T C L G Q Y T V S S N H N P L R
     LCK * H V L D S I L C H P T T I H * E
19681 - AGTTGTAGTTCCACAGGTTACTTGTACCATGCACCCTTCAACTTTGCCTGACGGGAATGC - 19740
    -SCSSTGYLYHAPFNFA*REC
    - V V P Q V T C T M H P S T L P D G N A
     L * F H R L L V P C T L Q L C L T G M P
-H F P K T T L Q N S R S D * C L W W L V
     IFLKPLCRTAEVIDVCGGW*
      FS*NHSAEQQK*LMSVVVGR
19801 - GAGAACATCAGCACCTGAGTTGCTAAAGTCATTTAGAGCCTTTGCTAAGTGGCAGCAAGC - 19860
    -ENIST * VAKVI * SLC * VAAS
    - R T S A P E L L K S F R A F A K W Q Q A
     E H Q H L S C * S H L E P L L S G S K L
19861 - TGCTTCACGATAGCTGGTAGTATCTAAGGCTCCACTGAAATACTTGTACTTGTTATATAG - 19920
    -C F T I A G S I * G S T E I L V L V I *
    - A S R * L V V S K A P L K Y L Y L L Y R
     L H D S W * Y L R L H * N T C T C Y I E
19921 - AGCAAGATACCTGTTATACTGTGTAAGTGGCAACAGTGTCTCGCTACGCAATTTTAGGTA - 19980
    -SKIPVILCKWQQCLATQF * V
    - A R Y L L Y C V S G N S V S L R N F R Y
      O D T C Y T V * V A T V S R Y A I L G T
19981 - CATTTCCTTGTTGAGCAAAAAGGTACACAAAGCAGCCTCCTCGAAGGTACTAAATGTAAC - 20040
    -HFLVEQKGTQSSLLEGTKCN
    - I S L L S K K V H K A A S S K V L N V T
      FPC * AKRYTKQPPRRY * M * L
20041 - TCCATTAAACATGACTCTTTTCCTAAGATAGTTGTTAAAGAACCAATGGCAGTGCTTCAG - 20100
    -SIKHDSFPKIVVKEPMAVLQ
     PLNMTLFLR*LLKNQWQCFR
      H * T * L F S * D S C * R T N G S A S E
20101 - AGAAATACAGAATACATAGATTGCTGTTATCCAAAAAGGCACAATAGGAGAAAACATGGC - 20160
    -RNTEYIDCCYPKRHNRRKHG
    - EIQNT * IA VIQKGTIGENMA
      KYRIHRLLLSKKAQ * EKTW Q
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20161 - AAACCATTGAAGGTGAGCCAAGAATGAAACATCATTGGTGAAATAGAATGTCAAGTACAA - 20220
    - K P L K V S Q E * N I I G E I E C Q V Q
   - N H * R * A K N E T S L V K * N V K Y K
      TIEGEPRMKHHW*NRMSSTS
-V K D * V D S R Q K A V S W Y Q T E Y S
     * K T E * T P G R K L * A G T R Q S I V
      KRLSRLPAESCKLVPDRV**
20281 - GAAAGACATCAAAAACAAAAGTGCATTAGCAGCAACAACATGGTTGTACTCACCAAAAAC - 20340
    -ERHQKQKCISSNNMVVLTKN
    - KDIKNKSALAATTWLYSPKT
      20341 - ACGTCTGAATTTCATAAAGTAGTAGGCAGCACAAGTCACCAATATGGCAATAATACCACC - 20400
    -TSEFHKVVGSTSHQYGNNTT
    - R L N F I K * * A A Q V T N M A I I P P
      V * I S * S S R Q H K S P I W Q * Y H Q
20401 - AGCCACTACTGAAGCAGACACATCTAAAGCACCCACAGGTTGCACAAGAGGAGTAAAGAT - 20460
    -SHY*SRHI*STHRLHKRSKD
    - A T T E A D T S K A P T G C T R G V K M
      PLLKQTHLKHPQVAQEE*RC
20461 - GTTAGCTATGAGATTCATCGCATCAACACCACAGAAAACTCCTGATAGAGCTCTGTAATG - 20520
    - V S Y E I H R I N T T E N S * * S S V M
    - L A M R F I A S T P Q K T P D R A L * C
      * L * D S S H Q H H R K L L I E L C N A
20521 - CTCATTATTAAGAACCCATCTACCACTGGTAGATAGGCAAATACCTACTTCTGACCTTTC - 20580
    -LIIKNPSTTGR*ANTYF*PF
    - S L L R T H L P L V D R Q I P T S D L S
      HY*EPIYHW*IGKYLLTFR
20581 - GCATGTACCATGTCTACAGTACTCAGCATCAAAAGTTGTTACTACTCTAACAGAACCCTC - 20640
    - A C T M S T V L S I K S C Y Y S N R T L
    - H V P C L Q Y S A S K V V T T L T E P S
       \begin{smallmatrix} M & Y & H & V & Y & S & T & Q & H & Q & K & L & L & L & L & & Q & N & P & P \\ \end{smallmatrix} 
20641 - CAGGTAAGTGTTAGGAAACTGTATGATGGAACCATCCATAAGCACATAACGAGTGTCTGG - 20700
    -Q V S V R K L Y D G T I H K H I T S V W
    - R * V L G N C M M E P S I S T * R V S G
      G K C * E T V * W N H P * A H N E C L D
20701 - ACGAAGCTCACTATAAGAAATAGAACCCTCTAGCAAATTAGTGTCATAACAATATGGCAC - 20760
    -TKLTIRNRTL * QISVITIWH
    - R S S L * E I E P S S K L V S * Q Y G T
      E A H Y K K * N P L A N * C H N N M A Q
20761 - AGGTTTGCCCATAGCATCCTTAAAAATTGTACACTCAGCAGCAAGAACGCAAGCAGGGT - 20820
    -RFAHSILKNCTLSSKNASRG
    - G L P I A S L K I V H S A A R T Q A E V
      V C P * H P * K L Y T Q Q E R K Q R *
20821 - AGCAAAATCACTATACTCAATGAGTTTGGAAGGTGTGTAGCAAATGTTGCCAACAGCACT - 20880
    -SKITILNEFGRCVANVANST
     A K S L Y S M S L E G V * Q M L P T A L
      ONHYTQ*VWKVCSKCCQQH
-KNTR*KMQEVTIDCSQHSTR
    - K T R G R K C K K S P L I A L S T V P G
      KHEVENARSHH*LLSAQYPV
20941 - TAAGCCAGGCACTATGAAACCAATCTCTCTTGTAATGATAGCAGCTACTACAGGGCAGCT - 21000
    - * A R H Y E T N L S C N D S S Y Y R A A
     K P G T M K P I S L V M I A A T T G Q L
      S O A L * N O S L L * * * O L L O G S F
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21001 - TTTGTCATTTTTGTATGAACCACCACGCTGGCTAAACCATGCGTCAAAACCAGCATGTTT - 21060
    -FVIFV*TTTLAKPCVKTSMF
    - L S F L Y E P P R W L N H A S K P A C L
      CHFCMNHHAG*TMRQNQHVY
21061 - ATTTGCAAAACAATCATCAGTAGAAATGATGTCACGAGTGACACCATCCTGAATGGCTTT - 21120
    -ICKTIISRNDVTSDTILNGF
    - FAKQSSVEMMSRVTPS * MAL
      L Q N N H Q * K * C H E * H H P E W L C
- V T N D F I C V T I M D * Q C M Y W H N - * P M I S F V * P S W I D N V C T G I T
      NQ * F H L C N H H G L T M Y V L A * R
21181 - GATATAACAAACCAATGCAGCAAGAACGCACAATAATGTGGCCTTAAGCATAAGTTTAAA - 21240
    -DITNQC'SKNAQ * CGLKHKFK
      I * Q T N A A R T H N N V A L S I S L K
       YNKPMQQERTIMWP*A*V*N
21241 - ACAAGTACTAACAATCTTACCACCCTTGAGTGAGATTTTAGTAGTATTATGACATTGACAAC - 21300
    -TSTNNLTTLE * DFSSYDIDN
    - Q V L T I L P P L S E I L V V M T L T T
      K Y * Q S Y H P * V R F * * L * H * Q P
21301 - CTGTCTAGTTGTAGCACAAGTTAGTGTAAAAGGTATGTTGTTCTTCTTGGCAGCAGTACG - 21360
    -L S S C S T S * C K R Y V V L L G S S T
    - C L V V A Q V S V K G M L F F L A A V R
       V * L * H K L V * K V C C S S W Q Q Y E
21361 - AATTTGTTTACGCAGCTGTTCAGATAAAGACATGTAGTCTTTTACATTCCAGATGAGTGA - 21420
    -NLFTQLFR*RHVVFYIPDE*
    - I C L R S C S D K D M * S F T F Q M S E
      FVYAAVQIKTCSLLHSR*VK
21421 - AACATTGTGACTTTTTGCTACTTGGGCATTGATATGCCTTGCATTACAGTCAATACATGC - 21480
    -NIVTFCYLGIDMPCITVNTC
    - T L * L F A T W A L I C L A L Q S I H A - H C D F L L L G H * Y A L H Y S Q Y M R
21481 - GCCAAGATCTCTGGGCGTCATGTTTTCAACCTTATTATAGGTGAGCATGAAATTGTTACA - 21540
    -AKISGRHVFNLIIGEHEIVT
    - PRSLGVMFSTLL*VSMKLLQ
- QDLWASCFQPYYR*A*NCYN
21541 - ACTGTCACCTGTCACTTCTAAGTCAGAGTGATGTGAAAGTTTGAGACATTCAATAACATC - 21600
    -TVTCHF*VRVM*KFETFNNI
    - L S P V T S K S E * C E S L R H S I T S
- C H L S L L S Q S D V K V * D I Q * H P
21601 - CTTTGTGTCAACATCGGTATCAACAACACCTTGTCGGGCAGCTGACACGAATGTAGAAAG - 21660
    -LCVNIGINNTLSGS*HECRK
    - F V S T S V S T T P C R A A D T N V E R
       L C Q H R Y Q Q H L V G Q L T R M * K G
21661 - GACACCATCTAAAGCTACACCCTTTGCTAACTCGCTGTGAGCTGTAGCAACAAGTGCCTT - 21720
    -D T I * S Y T L C * L A V S C S N K C L
    - T P S K A T P F A N S L * A V A T S A L
      H H L K L H P L L T R C E L * Q Q V P *
21721 - AAGTTTTTCCATAGGAACACTAAAAGTTGCTGAAAAGGTGTCGACATAAGCATCAAACAT - 21780
    -KFFHRNTKSC * KGVDISIKH
      S F S I G T L K V A E K V S T * A S N I
      V F P * E H * K L L K R C R H K H Q T S
21781 - CTTAACGGAAACTTCAGTACTATCTCCAACGTTTGATACAAGAGCTTGGTCAAGCAACAG - 21840
    -LNGNFSTISNV * YKSLVKQQ
     L T E T S V L S P T F D T R A W S S N R
      * R K L Q Y Y L Q R L I Q E L G Q A T E
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21841 - AATAGGTTGGCACATCAGCTGACTGTAGTACACAGAAGCAGACTTAGAAGCAGACTCGTC - 21900
    -N R L A H Q L T V V H R S R L R S R L V
      I G W H I S * L * Y T E A D L E A D S S
       * V G T S A D C S T Q K Q T * K Q T R R
21901 - GCATTTGGACTTGCCATCAAAAACTATGACATTAATAGGCAGTGAACCTTTAGTGTTGTT - 21960
    -AFGLAIKNYDINRQ*TFSVV
    - H L D L P S K T M T L I G S E P L V L L
       I W T C H Q K L * H * * A V N L * C C *
21961 - AGCTCTCAAATTGTCTAAATTGACAAAATGGGAGAGCGGATGTCTCTCATAGGTCTTTTG - 22020
    -SSQIV * I D K M G E R M S L I G L L
    - A L K L S K L T K W E S G C L S * V F *
      L S N C L N * Q N G R A D V S H R S F D
22021 - ACCAGCCTTGTCAAAGTAGAGGTGAAGCGCGCCATTTTTCACAGCAACACTATCAACAAT - 22080
    -T S L V K V E V K R A I F H S N T I N N
    - P A L S K * R * S A P F F T A T L S T I
       Q P C Q S R G E A R H F S Q Q H Y Q Q Y
22081 - ATACGATGACTGGTCAGTAGGGTTGATTGGTCTTTTAAACTGGAGTGACAAATCACGAGC - 22140
    - I R * L V S R V D W S F K L E * Q I T S
     Y D D W S V G L I G L L N W S D K S R A
       T M T G Q * G * L V F * T G V T N H E Q
22141 - AACTTCATCACTAATGAATGTACTACCAGTGCAAAATGTGTCACAATTGAGACAATTCCA - 22200
    -N F I T N E C T T S A K C V T I E T I P
     T S S L M N V L P V Q N V S Q L R Q F Q
      L H H * * M Y Y Q C K M C H N * D N S N
22201 - ATTGTGAGTCTTGCAGAAGCCACGGCCTCCATTTGCATAGACATAGAAAGATCTCTTCAT - 22260
    -I V S L A E A T A S I C I D I E R S L H
     L * V L Q K P R P P F A * T * K D L F M
       C E S C R S H G L H L H R H R K I S S C
22261 - GCCATTAACAATAGTTGTACACTCAACGCGTGTGGCACGATTGCGCTTATAGCACATCAT - 22320
    -AINNSCTLNACGTIALIAHH
     PLTIVVHSTRVARLRL*HIM
       22321 - GCAAGTCGAAGAGGTGCAACCATCCATGATATGAACATAGCTCTTCCATATGTAGTAGAA - 22380
    - A S R R G A T I H D M N I A L P Y V V E
       \verb"Q" V E E V Q P S M I * T * L F H M * * K \\
       K S K R C N H P * Y E H S S S I C S R K
22381 - AGAAGCAAAGAAGATGTACATCCTAACCATTGCAGAAACGGGTGCCATTTGTACAATACT - 22440
    -RSKEDVHPNHCRNGCHLYNT
     E A K K M Y I L T I A E T G A I C T I L
       K Q R R C T S * P L Q K R V P F V Q Y *
22441 - AATGATAAACCACATGAGCCAAGAATTGCTGATGAAATGACTAGCAAAAATAGCCAAAGAA - 22500
    -N D K P H E P R I A D E M·T S K I A K E
     M I N H M S Q E L L M K * L A K * P K N * * T T * A K N C * * N D * Q N S Q R T
22501 - CACCTGCATTATAGCTGAAAGACCTAATAAATAAAAGAATTTTGTGAACAACATATATGC - 22560
    CIIAERPNK * KNFVNNIYA
       PAL*LKDLINKRIL*TTYMP
22561 - CAAAACCCACTCAGCGGCCAGACCTAAAATTGTCAAGTCTAGCTTGTACGATGAAATCGT - 22620
    -QNPLSGQT * NCQV * LVR * NR
     K T H S A A R P K I V K S S L Y D E I V
       K P T Q R P D L K L S S L A C T M K S S
22621 - CACCTGAATGGTTTCAAGAGCTGGATAAGAATCAAGGGAGTCTAATCCACTTAAACAAAT - 22680
    -HLNGFKSWIRIKGV*ST*TN
     T * M V S R A G * E S R E S N P L K Q M
       PEWFQELDKNQGSLIHLNKC
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22681 - GCTGCAAGGAAAAGAACCTTCACAGAAATCCATAGTAGTAACGTTAGACGAATTAAGATA - 22740
    - A A R K R T F T E I H S S N V R R I K I
   - L Q G K E P S Q K S I V V T L D E L R Y
     C K E K N L H R N P * * * R * T N * D T
22741 - CAATTCTCTAACGCCATTACAATAAGAAGGAGCACCAAAATTAGATAAGAGTACACCAAA - 22800
    -QFSNAITIRRSTKIR*EYTK
     N S L T P L Q * E G A P K L D K S T P K
      IL*RHYNKKEHQN*IRVHQK
22801 - AGCAGCAGTTACACAGATTAGAGAACCTAAGCAAATACTTAACAACAATAGCCACATAGC - 22860
    - A A V T Q I R E P K Q I L N N N S H I A
      Q Q L H R L E N L S K Y L T T I A T * R
-DCEQFRKFG * L H I I N A G I Q T
   - I V N N L E N L G D F T * L M P A S K H
      L * T I * K I W V T S H N * C R H P N I
- * F S N T L N T I F S N S C R * * S S N
   - N L A T L L T L F L A I V V G S E A L I
      I * Q H S * H Y F * Q * L * V V K L * F
22981 - TCTAGAATTGGTACTTTTAGTAAAAGTACACAATTGGAACAATAATGTAAACACATAAGG - 23040
    -SRIGTFSKSTQLEQ*CKHIR
    - L E L V L L V K V H N W N N N V N T * G
      * N W Y F * * K Y T I G T I M * T H K A
23041 - CATATAATTGTTAAACACACGTTGTGCTAATCTCTTAGCGCAATTTGATGTTGTAATTGC - 23100
    -HIIVKHTLC * SLSAI * CCNC
    I * L L N T R C A N L L A Q F D V V I A
      YNC * THVVLIS * RNLML * LL
23101 - TGCTTGTCCTAAGAATGGTTTGACATAAGCCAAAATTTTACTCCAAGGAACACTATTAAT - 23160
    -CLS * E W F D I S Q N F T P R N T I N
    - A C P K N G L T * A K I L L Q G T L L I
     L V L R M V * H K P K F Y S K E H Y * L
23161 - TGCAGCAATACCATGAGTGGCAATTGTTTTTAAACCTAAGGCTAGTGAAAGCTCATTAGG - 23220
    - A A I P * V A I V F K P K A S E S S L G
     QQYHEWQLFLNLRLVKAH*V
23221 - TTTCTTAATGGTAATGCTTGTGTTTTCCACATAAGCAGCCATAAGATCCTCATGACCTAA - 23280
    -FLNGNACVFHISSHKILMT*
    - F L M V M L V F S T * A A I R S S * P N
      S * W * C L C F P H K Q P * D P H D L T
23281 - CTCTTGTGTTACTTTAACACCTTCATCTGATGGTTTAAGTATGACATTGCCTACAACTTC - 23340
    -LLCYFNTFI * W F K Y D I A Y N F
     S C V T L T P S S D G L S M T L P T T S
      LVLL * H L H L M V * V * H C L Q L R
23341 - GGTAGTTTTCACGTCACACTCTATGACTTCCTTCTGTATGGTAGGATTTTCCACTACTTC - 23400
    -G S F H V T L Y D F L L Y G R I F H Y F
     V V F T S H S M T S F C M V G F S T T S
     * F S R H T L * L P S V W * D F P L L L
23401 - TTCAGAGGTGGGTTGTTGACTTTCACAAGCAAGATTGTCCATTCCTTGTGTGTCTTCTAC - 23460
    -FRGGLLTFTSKIVHSLCVFY
     SEVGC*LSQARLSIPCVSST
      Q R W V V D F H K Q D C P F L V C L L L
23461 - TGCCAGAACTTCAAATGAATTTGAAGTATCTACTGGCTTTGTACTCCAAAGACAACGTAA - 23520
    -CQNFK*I*SIYWLCTPKTT*
     ARTSNEFEVSTGFVLQRQRK
      P E L Q M N L K Y L L A L Y S K D N V N
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23521 - ACACCAAGTGTTTGGTTTGAACGTTGTCTTGGTTGTAGCCTGGTTAATGTGCCAAACAAT - 23580
    -TPSVWFERCLGCSLVNVPNN
    - H Q V F G L N V V L V V A W L M C Q T I
- T K C L V * T L S W L * P G * C A K Q L
23581 - TGGCTTATGCAGTAATTTAGCACCTTTCTTGAAACTCGCTGAATAGTGTCTATAGTCAAT - 23640
    -W L M Q * F S T F L E T R * I V S I V N
    - G L C S N L A P F L K L A E * C L * S I
       A Y A V I * H L S * N S L N S V Y S Q *
23641 - AGCCACTACATCGCCATTCAAGTCTGGGAAGAATGTGACAGATAGCTCTCGTGAAGCTGG - 23700
    -SHYIAIQVWEECDR*LS*SW
    - A T T S P F K S G K N V T D S S R E A G
       PLHRHSSLGRM * QIALVKLA
23701 - CTTTGTGAAGCCTGTCATTTGATTTAAATCATCAGCAAATTTTGTGTTAGAACATGTGAG - 23760
    -LCEACHLI*IISKFCVRTCE
    - F V K P V I * F K S S A N F V L E H V S
      L * S L S F D L N H Q Q I L C * N M * V
23761 - TTTGAAATTATCAAAACTCGCATTTGGTAATGGTTGAGTTGGTACAAGGTCTATAGGCTG - 23820
    -FEIIKTRIW * W L S W Y K V Y R L
    - L K L S K L A F G N G * V G T R S I G C
      * N Y Q N S H L V M V E L V Q G L * A A
23821 - CTCTGTATAGTAAGCATTATCCTTTTTATAATACCCATCCAATTTTGGTTCAATCTCTGT - 23880
    -LCIVSIILFIIPIQFWFNLC
      S V * * A L S F L * Y P S N F G S I S V
      LYSKHYPFYNTHPILVQSLC
23881 - GTAAGTAACTCCATCGAGTTTATACGACACAGGCTTGATGGTTGTAGTGTAAGATGTTTC - 23940
    - V S N S I E F I R H R L D G C S V R C F
    - * V T P S S L Y D T G L M V V V * D V S
       K * L H R V Y T T Q A * W L * C K M F P
23941 - CTTGTAGAAAACATCAGTCACTGGTCCTTTGTACTCTGACATCTTTGTAAGGTGAGCTCC - 24000
    -L V E N I S H W S F V L * H L C K V S S
    - L * K T S V T G P L Y S D I F V R * A P
       C R K H Q S L V L C T L T S L * G E L R
24001 - GTCAATACGATAGAGGGTCTCCTTAGCAGTTATATGAGTGTAATGACCACACTGATAGTT - 24060
    -V N T I E G L L S S Y M S V M T T L I V
    - S I R * R V S L A V I * V * * P H * * L
      Q Y D R G S P * Q L Y E C N D H T D S Y
24061 - ACCAGTGTACTCATTCGCACATAAGAATGTACCTTGCTGTAATTTATACTCAGCAGGTGG - 24120
    -TSVLIRT*ECTLL*FILSRW
    - P V Y S F A H K N V P C C N L Y S A G G
      Q C T H S H I R M Y L A V I Y T Q Q V V
24121 - TGCAGACATCATAACAAAAGAAGACTCTTGTTGTACTAGATATTGTGTAGCATCACGACC - 24180
    -CRHHNKRRLLLY*ILCSITT
    - A D I I T K E D S C C T R Y C V A S R P
      QTS*QKKTLVVLDIV*HHDH
24181 - ACACACATGGAATGGAAACACCTGTCTTAAGATTATCATAAGATAGAGTACCCATATA - 24240
    -THTWNGNTCLKIIIR*STHI
    - H T H G M E T P V L R L S * D R V P I Y - T H M E W K H L S * D Y H K I E Y P Y T
24241 - CATCACAGCTTCTACACCCGTTAAGGTAGTAGTTTTCTGACCACAATGTTTACACACCAC - 24300
    - H H S F Y T R * G S S F L T T M F T H H
- I T A S T P V K V V V F * P Q C L H T T
       SQLLHPLR * * F S D H N V Y T P H
24301 - ATTAAGAACTCGCTTTGCAGATTCCAAATTAGCATGCTGTAGAAGATGGGTCATAGTTTC - 24360
    -IKNSLCRFQISML*KMGHSF
     L R T R F A D S K L A C C R R W V I V S
        ELALQIPN * HAVEDGS * FL
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24361 - TCTGACATCACCAAGCTCGCCAACAGTTTTATTACTGTAAGCGAGTATGAGTGCACAAAA - 24420
    -SDITKLANSFITVSEYECTK
    - L T S P S S P T V L L L * A S M S A Q K
      * H H Q A R Q Q F Y Y C K R V * V H K S
24421 - GTTAGCAGCATCACCAGCACGGGCTCTATAATAAGCCTCTTGAAGTGCTGGTGCATTGAA - 24480
    -VSSITSTGSIISLLKCWCIE
      L A A S P A R A L * * A S * S A G A L N
      * Q H H Q H G L Y N K P L E V L V H * I
24481 - TTTGACTTCAAGCTGTTGAAGTGCTAATAAAACACTAGACAAATAACAATTGTTATCAGC - 24540
    -FDFKLLKC * * N T R Q I T I V I S
    - L T S S C * S A N K T L D K * Q L L S A
      * L Q A V E V L I K H * T N N N C Y Q P
24541 - CCATTTAATTGAAGTTAAACCACCAACTTGAGGAAATTTCCATTTCTTTGTGTGGTTTAA - 24600
    -PFN * S * TTNLRKFPFLC V V *
    - H L I E V K P P T * G N F H F F V W F K
       I * L K L N H Q L E E I S I S L C G L K
24601 - AGCAGACATGTACCTACCAAGAAAACTCTCATCAAGAGTATGGTAGTACTCGAAAGCTTC - 24660
    -SRHVPTKKTLIKSMVVLESF
    - A D M Y L P R K L S S R V W * Y S K A S
      Q T C T Y Q E N S H Q E Y G S T R K L H
24661 - ACTACGTAGTGTCATCACTAGGTAGTACAAAGAAAGTCTTACCCTCATGATTTACATG - 24720
    -TT * C V I T R * Y K E S L T L M I Y M
    - L R S V S S L G S T K K V L P S * F T *
      Y V V C H H * V V Q R K S Y P H D L H E
24721 - AGGTTTAATTTTTGTAACATCAGCACCATCCAAGTATGTTGGACCAAACTGCTGTCCATA - 24780
    -R F N F C N I S T I Q V C W T K L L S I
    - G L I F V T S A P S K Y V G P N C C P Y
      V * F L * H Q H H P S M L D Q T A V H M
24781 - TGTCATAGACATATCCACAAGCTGTGTGTGGAGATTAGTGTTGTCCACAGTTGTGAACAC - 24840
    -CHRHIHKLCVEISVVHSCEH
    - V I D I S T S C V W R L V L S T V V N T
       S * T Y P Q A V C G D * C C P Q L * T L
24841 - TTTTATAGTCTTAACCTCCCGCAGGGATAAGAGACTCTTTAGTTTGTCAAGTGAAAGAAC - 24900
    -FYSLNLPQG*ETL*FVK*KN
    - FIVLTSRRDKRLFSLSSERT
      L * S * P P A G I R D S L V C Q V K E P
24901 - CTCACCGTCAAGATGAAACTCGACGGGGCTCTCCAGAGTGTGGTACACAATTTTGTCACC - 24960
    -L T V K M K L D G A L Q S V V H N F V T
     S P S R * N S T G L S R V W Y T I L S P
      H R Q D E T R R G S P E C G T Q F C H H
24961 - ACGCTTAAGAAATTCAACACCTAACTCTGTACGCTGTCCTGAATAGGACCAATCTCTGTA - 25020
    -TLKKFNT * LCTLS * IGPIS V
    - R L R N S T P N S V R C P E * D Q S L *
      A * E I Q H L T L Y A V L N R T N L C K
25021 - AGAGCCAGCCAAAGAAACTGTTTCTACAAAGTGCTCCTCAGATGTCTTTGATGACGAAGT - 25080
    -RASQRNCFYKVLLRCL**RS
     E P A K E T V S T K C S S D V F D D E V
       SQPKKLFLQSAPQMSLMTK*
25081 - GAGGTATCCATTATATGTAGTAACAGCATCTGGTGATGATACTGACACTACGGCAGGAGC - 25140
    -EVSIICSNSIW**Y*HYGRS
     RYPLYVVTASGDDTTTAGA
      G I H Y M * * Q H L V M I L T L R Q E L
25141 - TTTAAGAGAACGCATACAGCGCGCGCCTCTTCAAGATTAAAACCATGTGTCACATAACC - 25200
    -F K R T H T A R S L F K I K T M C H I T
     L R E R I Q R A A S S R L K P C V T * P
       ENAYSAQPLQD*NHVSHNQ
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25201 - AATTGGCATTGTGACAAGCGGCTCATTTAGAGAGTTCAGCTTCGTAATAATAGAAGCTAC - 25260
    -NWHCDKRLI*RVQLRNNRSY
    - I G I V T S G S F R E F S F V I I E A T
       LAL*QAAHLESSAS***KLQ
25261 - AGGCTCTTTACTAGTATAAAAGAAGAATCGGACACCATAGTCAACGATGCCCTCTTGAAT - 25320
    -RLFTSIKEESDTIVNDALLN
    - G S L L V * K K N R T P * S T M P S * I
       ALY*YKRRIGHHSQRCPLEF
25321 - TTTAATTCCTTTATACTTACGTTGGATGGTTGCCATTATGGCTCTAACATCCATGCATAT ~ 25380
    -FNSFILTLDGCHYGSNIHAY
    - L I P L Y L R W M V A I M A L T S M H I
       * F L Y T Y V G W L P L W L * H P C I *
25381 - AGGCATTAATTTTCTTGTCTCTTCAGCATGAGCAAGCATTTCTCTCAAATTCCAGGATAC - 25440
    -RH * F S C L F S M S K H F S Q I P G Y
    - G I N F L V S S A * A S I S L K F Q D T
       A L I F L S L Q H E Q A F L S N S R I Q
25441 - AGTTCCTAGAATCTCTTCCTTAGCATTAGGTGCTTCTGAAGGTAGTACATAAAATGCAGA - 25500
    -SS * N L F L S I R C F * R * Y I K C R
    - V P R I S S L A L G A S E G S T * N A D - F L E S L P * H * V L L K V V H K M Q I
25501 - TTTGCATTTCTTAAGAGCAGTCTTAGCTTCCTCAAGTGTATAACCAGCACATCCTTGTCC - 25560
    -FAFLKSSLSFLKCITSTSLS
    - L H F L R A V L A S S S V * P A H P C P - C I S * E Q S * L P Q V Y N Q H I L V Q
25561 - AGGGTACGTGGTTATATACTCATCAACTGGCACTTTCTTCAAAGCTCTTGAGAGCATCTC - 25620
    -RVRGYILINWHFLQSS*EHL
    - G Y V V I Y S S T G T F F K A L E S I S
       G T W L Y T H Q L A L S S K L L R A S Q
25621 - AGTAGTGCCACCAGCCTTTTTGGAGGGTATTACAACACAAGTGATATCACCACTAGTGAT - 25680
    -SSATSLFGGYYNTSDITTSD
     V V P P A F L E G I T T Q V I S P L V I
       * C H Q P F W R V L Q H K * Y H H * *
25681 - AACATCACCTACCATGTAAGGTGCATCCTTCTCAAGGAAAGACATATCTTCACCTCTAAG - 25740
    -NITYHVRCILLKERHIFTSK
    - T S P T M * G A S F S R K D I S S P L S
       H H L P C K V H P S Q G K T Y L H L * A
25741 - CATGTTCTGAGAATCATGGTAAAGCTTACCATTGATATCAGCAAACAAGAGTAACTTATT - 25800
    -HVLRIMVKLTIDISKQE*LI
     M F * E S W * S L P L I S A N K S N L L
C S E N H G K A Y H * Y Q Q T R V T Y W
25801 - GGTAAGAAACTTAGTTTCTTCCAGTGTTGTGGTAACCTCATCAATGCAGGCCTTAATTTT - 25860
    -G K K L S F F Q C C G N L I N A G L N F
     V R N L V S S S V V V T S S M Q A L I F
* E T * F L P V L W * P H Q C R P * F L
25861 - TGGCTTCACATCGACAGGCTTCTGTACGACAGATTTCTCCTCAGTTTTGGAATCTTCTGT - 25920
    -WLHIDRLLYDRFLLSFGIFC
    - G F T S T G F C T T D F S S V L E S S V
      A S H R Q A S V R Q I S P Q F W N L L C
25921 - GTTTGGTGGCTCCTCTTGTTTAGGTGCTTCCACTCTAGGCTTCAGGTTATCAAGATAATC - 25980
    -V W W L L L F R C F H S R L Q V I K I I
     F G G S S C L G A S T L G F R L S R * S
       L V A P L V * V L P L * A S G Y Q D N P
25981 - CATGACAACCTGCTCATAAAGAGCTTTGTCATTGACTGCAATATAAACCTGTGTACGAAC - 26040
    - H D N L L I K S F V I D C N I N L C T N
     MTTCS*RALSLTAI*TCVRT
        Q P A H K E L C H * L Q Y K P V Y E P
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26041 - CGTCTGCACGCACACTTGTAAAGACTGAAGTGGTTTAGCACCAAATATGCCTGCTGACAA - 26100
    -RLHAHL*RLKWFSTKYAC*Q
     V C T H T C K D * S G L A P N M P A D N
       SARTLVKTEVV * HQICLLTT
26101 - CAATGGTGCAAGTAAGATGTCCTGTGAATTGAAATTTTCATATGCTGCCTTAAGAAGCTG - 26160
    -Q W C K * D V L * I E I F I C C L K K L
      N G A S K M S C E L K F S Y A A L R S W
       M V Q V R C P V N * N F H M L P * E A G
26161 - GATGTCCTCACCTGCATTTAGGTTAGGTCCAACAACATGCAGACACTTCTTAGCAAGATT - 26220
    -DVLTCI * VRSNNMQTLLSKI
    - M S S P A F R L G P T T C R H F L A R L
       C P H L H L G * V Q Q H A D T S * Q D Y
26221 - ATGTCCAGAAAGCAAACAAGACCCTCCTACTGTAAGAGGGCCATTTAGCTTAATGTAATC - 26280
    - M S R K Q T R P S Y C K R A I * L N V I
      C P E S K Q D P P T V R G P F S L M * S
       V Q K A N K T L L L * E G H L A * C N H
26281 - ATCACTCTCTTTTGCATGGCACCATTGGTTGCCTTGTTGAGTGCACCTGCTACACCACC - 26340
    -I T L L H G T I G C L V E C T C Y T T
    - S L S F C M A P L V A L L S A P A T P P
       HSPFAWHHWLPC*VHLLHHH
26341 - ACCATGTTTCAGGTGTATGTTAGCAGCATTTACAATCACCATAGGATTAGCACTTTGTGC - 26400
    -TMFQVYVSSIYNHHRISTLC
    - P C F R C M L A A F T I T I G L A L C A - H V S G V C * Q H L Q S P * D * H F V P
26401 - CTCCTTAACGATGTCAACACATTTAATGGCAACATTGTCAGTAAGTTTTAAATAACCAGT - 26460
    -LLNDVNTFNGNIVSKF*ITS
       \verb|SLTMSTHLMATLSVSFK*PV| \\
       P * R C Q H I * W Q H C Q * V L N N Q *
26461 - AAACTGATTAACTGGTTCTTCAGGTGTAGGTTCTGGTTCTGGCTCAATCTCTGATTGCTC - 26520
    -KLINWFFRCRFWFWLNL*LL
      N * L T G S S G V G S G S G S I S D C S
T D * L V L Q V * V L V L A Q S L I A Q
26521 - AGTAGTATCATCCAGCCAGTCTTCCTCTTCTTCTTCCTCAACTCGAACTGTTTCAGCTGA - 26580
    -SSIIQPVFLFFFLNSNCFS*
      V V S S S Q S S S S S S S T R T V S A E
       * Y H P A S L P L L P Q L E L F Q L R
26581 - GGCACCAAATTCCAGAGGGAGACCTTGATAATCATCCTCTGTACCGTACTCATGTTCACA - 26640
    -GTKFQRETLIIILCTVLMFT
-APNSRGRP**SSSVPYSCSQ
       H Q I P E G D L D N H P L Y R T H V H R
26641 - GGTTTCATCAATTTCTTCTTCCTCACACTCTGCATCGTCCTCTTCTTCCTCATCTGGAGG - 26700
    -GFINFFFLTLCIVLFFLIWR
      V S S I S S S S S S S S S S G G
       F H Q F L L P H T L H R P L L P H L E G
26701 - GTAAAAGGAACAATACATACGTGATGAAAAGTTTTCTTCACCAGCATCATCAAATAAGTA - 26760
    -V K G T I H T * * K V F F T S I I K * V
        KEQYIRDEKFSSPASSNK*
       K R N N T Y V M K S F L H Q H H Q I S R
26761 - GAATGTAGCTACACTCACTCATCAAGATCAATACCCATGTTGGTAAGGAGATCAGAAAC - 26820
    -E C S Y T P L I K I N T H V G K E I R N
      N V A T L H S S R S I P M L V R R S E T
M * L H S T H Q D Q Y P C W * G D Q K L
26821 - TGGTTGTAAAGTCTTCACAACAGCCTCTGCTACAACACATGCAAACTCAGTAACTTCGGT - 26880
    -W L * S L H N S L C Y N T C K L S N F G
     G C K V F T T A S A T T H A N S V T S V
       V V K S S Q Q P L L Q H M Q T Q * L R Y
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26881 - ACCGGATTCAACAGTGTAGACAGAGCACTTTTCATTAAGCACTTTGTCAACACGTTCATC - 26940
    - T G F N S V D R A L F I K H F V N T F I
- P D S T V * T E H F S L S T L S T R S S
- R I Q Q C R Q S T F H * A L C Q H V H Q
26941 - AAGCTCAAATGTGATTCTCACATTCTTGTAACCTTGAACTTCCCAAACAGTATCTTCTCC - 27000
    A Q M * F S H S C N L E L P K Q Y L L Q
-KGYTFNWCTPF*AKDIVCSQ
    - K V T P L I G A P P F K R K T L F V A S
      RLHL*LVHPLLSERHCL*PV
27061 - TAAACCAGGAGACAATGCGCAGTATTGTTCTTTGTCCTTAATCTCTAAGAGCATGAGGCC - 27120
    - * T R R Q C A V L F F V L N L * E H E A
    - K P G D N A Q Y C S L S L I S K S M R P
      N Q E T M R S I V L C P * S L R A * G H
27121 - ATTTACACAGACTGGTGTGCCGACGATAGCTCCATTTGTGAAGCTATCAACGGGCGTCTC - 27180
    -IYTDWCADDSSICEAINGRL
    - F T Q T G V P T I A P F V K L S T G V S
       L H R L V C R R * L H L * S Y Q R A S R
27181 - GAGTGCTTCGAGTTCACCGTTCTTGAGAACAACCTCCTCAGAGGTAAGTACTGTGTCATG - 27240
    -ECFEFTVLENNLLRGKYCVM
      S A S S P F L R T T S S E V S T V S C
      V L R V H R S * E Q P P Q R * V L C H V
27241 - TGAATCACCTTCAAGAAAGGTTACTTCTTTTGGTGCCTTAAGAGGCATGAGTAGTTGCAG - 27300
    - * I T F K K G Y F F W C L K R H E * L Q
    - E S P S R K V T S F G A L R G M S S C S
      N H L Q E R L L L V P * E A * V V A A
27301 - CTGCTCCTTGCCACGTATACACTGACGGTAAAGTCCCTTGCTTTGAGCGATGAAGACTTC - 27360
    -LLLATYTLTVKSLALSDEDF
    - C S L P R I H * R * S P L L * A M K T S
       A P C H V Y T D G K V P C F E R * R L H
27361 - ACCTAAGTTGAGTGATCGCAACTTTGCGCCAGCGATAGTGACTTGATCAATGCACATTTC - 27420
    -T * V E * S Q L C A S D S D L I N A H F
    - P K L S D R N F A P A I V T * S M H I S
      LS * VIATLRQR * * LDQCTFR
27421 - GAGTGCCTTGTTAACAACATCAATGAAGCATTTTACACAATCCTTGATGTTATCTGAAGC - 27480
    -ECLVNNINEAFYTILDVI*S
      S A L L T T S M K H F T Q S L M L S E A
       V P C * Q H Q * S I L H N P * C Y L K Q
27481 - AACCTGTATTTGACCCTTGACGATGTCAAAAACACCTGTAATGAGAAATTTGAGAATCTC - 27540
    -NLYLTLDDVKNTCNEKFENL
    - T C I * P L T M S K T P V M R N L R I S
       PVFDP*RCQKHL**EI*ESP
27541 - CCAAGCATCCTTGAGAAATTCAACTCCTGCACTAAGTTTCGCCTCAATCCATTCAAAGAT - 27600
    -PSILEKFNSCTKFRLNPFKD
      Q A S L R N S T P A L S F A S I H S K I K H P * E I Q L L H * V S P Q S I Q R *
27601 - AGGCCTGAGTTTTTCAACAGTAGTGCCCAAAAGATTAGACAACCACTGAGAAGTCTGTTG - 27660
    -RPEFFNSSAQKIRQPLRSLL
      G L S F S T V V P K R L D N H * E V C C
       A * V F Q O * C P K D * T T E K S V V
27661 - TACAAGACCACCAGTTACATATGCCATAATAATGACACTGTTGGTGAGCAGGTCTGAAGT - 27720
    -Y K T T S Y I C H N N D T V G E Q V * S
       R P P V T Y A I I M T L L V S R S E V
       Q D H Q L H M P * * * H C W * A G L K Y
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27721 - ATAAACCATGGCGTCGACAAGACGTAATGACTGTTCAGAAATACCATCAAGTATGGTGAC - 27780
    -INHGVDKT**LFRNTIKYGD
     * T M A S T R R N D C S E I P S S M V T
      KPWRRQDVMTVQKYHQVW*Q
27781 - AGCTGCTCTTTGCAAATCAGGAATTGAGTGGTTTGCTGCATCAAGTGTGCGCGCAAAAAT - 27840
    -SCSLQIRN * V V C C I K C A R K N
    - A A L C K S G I E W F A A S S V R A K I
      L L F A N Q E L S G L L H Q V C A Q K L
27841 - TGATCTGATAACACCAGCAGCCTGTGAGGGAAAACCACAGTGGTGTTAAAACTGATCT - 27900
    - * S D N T S S L * G K T T Q W C * N * S
     D L I T P A A C E G K P H S G V K T D L
      I * * H Q Q P V R E N H T V V L K L I S
27901 - CTGTTGTCCAATGTTCCAAGCACCTTTTACGGGCTTTCCCTTGGTAACTTTATAGTTACC - 27960
    -LLSNVPSTFYGLSLGNFIVT
    CCPMFQAPFTGFPLVTL*LP
      V V Q C S K H L L R A F P W * L Y S Y R
27961 - GCAGGACTCAACAATGGTTTTGAAAGACTTGTAATCAAGACTCTTTATAGTGTCAATAAA - 28020
    -AGLNNGFERLVIKTLYSVNK
    - Q D S T M V L K D L * S R L F I V S I K
      R T Q Q W F * K T C N Q D S L * C Q * R
-GTCRSRERCQNDGNLFIQMK
    - A L V E A E K D A K M M A T S S F K * K
      HL * K Q R K M P K * W Q P L H S N E N
28081 - ATCGCCAACAATGTTAATGTTAACACGTTCACGACTCAGTATCTCAAGGAGATCCTCATT - 28140
    -IANNVNVTFTTQYLKEILI
    - S P T M L M L T R S R L S I S R R S S F
      R Q Q C * C * H V H D S V S Q G D P H S
28141 - CAAGGTCTCCACATTGTCACCAGTAATGCCAGTATGGCCTGAGCCAATATCAGCACTAGC - 28200
    - O G L H I V T S N A S M A * A N I S T S
    - K V S T L S P V M P V W P E P I S A L A
      R S P H C H Q * C Q Y G L S Q Y Q H * H
-TRNPVGTLIIAANIGKHTAS
    - R G T Q * A R L L * Q P T * A N T Q P P
      E E P S R H A Y Y S S Q H R Q T H S L Q
28261 - AAAACATCTAGTCCTACCTCCCTTGCGGAGTCGAGTTTCAATGTTTGAGTGGTTGTGATA - 28320
    - K T S S P T S L A E S S F N V * V V I
    - K H L V L P P L R S R V S M F E W L * *
       \verb|N I + S Y L P C G V E F Q C L S G C D N | \\
-I C N T M L R S N L W V L T G R T W H F
     SATLCSGPISGS*QAGHGIF
      L Q H Y A Q V Q S L G L D R Q D M A F S
28381 - CACTACAGCATTAGTAGGTAGGTACCCACATGTAGTAGGTCCTTCAATAACTAAATTTTC - 28440
    -HYSISR*VPTCSRSFNN*IF
     TTALVGRYPHVVGPSITKFS
LQH**VGTHM**VLQ*LNFQ
28441 - AGTGCCACAATGTTCACAAGTGGCTTTCAGAAAGTCGCACGTCTGCCATGAAACTTCATC - 28500
    -SATMFTSGFQKVARLP*NFI
    - V P Q C S Q V A F R K S H V C H E T S S
      CHNVHKWLSESRTSAMKLHR
28501 - GCAATGATTACATTTCATCAAGGTAGACAAGTGCATATTGTTACACTCCTGTGGAGATGC - 28560
    -AMITFHQGRQVHIVTLLWRC
     Q * L H F I K V D K C I L L H S C G D A
      N D Y I S S R * T S A Y C Y T P V E M O
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28561 - AACAGGGTACACAGAGCGTATACGCCCCATGAAACCCTCAGTCTTTTTCTTTTCAACACG - 28620
    -NRVHRAYTPHETLSLFNT
    - T G Y T E R I R P M K P S V F F F S T R
       Q G T Q S V Y A P * N P Q S F S F Q H V
28621 - TGGTTGAATGACTTTGACTTTTGAGTTAAGAGGAAACACAAACTTTGGGCATTCCCCTTT - 28680
    -WLNDFDF * VKRKHKLWAFPF
      {\tt G} \ \ {\tt M} \ \ {\tt T} \ \ {\tt L} \ \ {\tt T} \ \ {\tt F} \ \ {\tt E} \ \ {\tt L} \ \ {\tt R} \ \ {\tt G} \ \ {\tt N} \ \ {\tt T} \ \ {\tt N} \ \ {\tt F} \ \ {\tt G} \ \ {\tt N} \ \ {\tt F} \ \ {\tt L}
       VE * L * L L S * E E T Q T L G I P L *
28681 - GAAAGTGTCAAATTTCTTGGCACTCTTAATTTCGAAGGGTGTCTGGTGCTCGTAGCTCTT - 28740
    -ESVKFLGTLNFEGCLVLVAL
    - K V S N F L A L L I S K G V W C S * L L
       KCQISWHS*FRRVSGARSSY
28741 - ATCAGAGCGCTCAGTGAACCAGGCAATTTCATGCTCATGGTCACGGCAGCAGTAGACACC - 28800
    -IRALSEPGNFMLMVTAAVDT
    - S E R S V N Q A I S C S W S R Q Q * T P
       Q S A Q * T R Q F H A H G H G S S R H L
28801 - TCTCTTCGACTCGATGTAATCAAGTTGTTCGGAAAGAGTGCACATTGACTTGCCCGCGCG - 28860
    -S L R L D V I K L F G K S A H * L A R A
    - L F D S M * S S C S E R V H I D L P A R
       S S T R C N Q V V R K E C T L T C P R V
28861 - TGCGAGAAAATCTTTGATGCAATCAAGAGGGTACCCATCTGGGCCACAGAAATTGTTGTC - 28920
    -CEKIFDAIKRVPIWATEIVV
    - A R K S L M Q S R G Y P S G P Q K L L S
       RENL * CNQEGTHLGHRNCCR
-DIASDCTSIELTSEFTECTT
      T * R V T A P P L S S R V S S R S A P L
       HSE*LHLH*AHE*VHGVHHC
28981 - GCCATGCTTAGTGTTCCAGTTTTGTTCATAATCTTCAATGGGATCAGTGCCAAGCTCGTC - 29040
    -AMLSVPVLFIIFNGISAKLV
     PCLVFQFCS*SSMGSVPSSS
       HA * C S S F V H N L Q W D Q C Q A R H
29041 - ACCTAAGTCATAAGACTTTAGATCGATGCCATAGCTATGACCACCGGCTCCCTTATTACC - 29100
    -T * V I R L * I D A I A M T T G S L I T
     PKS * DFRSMP * L * PPAPLLP
       L S H K T L D R C H S Y D H R L P Y Y R
29101 - GTTCTTACGAAGAACATTGCGGTATGCAATTGGGGTTTCGCCCACATGTGGCACGAG - 29160
    -V L T K K N I A V C N W G F A H M W H E
     F L R R R T L R Y A I G V S P T C G T S
       S Y E E E H C G M Q L G F R P H V A R V
29161 - TACTCCCAGTGTTATACCGCTACGACCGTACTGAATGCCGTCCATTTCTGCAACCAGCTC - 29220
    - Y S Q C Y T A T T V L N A V H F C N Q L
     T P S V I P L R P Y * M P S I S A T S S
       L P V L Y R Y D R T E C R P F L Q P A Q
29221 - AACGACCTTGTGGCCGTGATTGGTGCTTAAGGCATCAGAACGTTTAATGAACACATAGGG - 29280
    -NDLVAVIGA*GIRTFNEHIG
     TTLWP*LVLKASERLMNT*G
RPCGRDWCLRHQNV**THRA
29281 - CTGTTCAAGCTGGGGCAGTACGCCTTTTTCCAGCTCTACTAGACCACAAGTGCCATTTTT - 29340
    -L F K L G Q Y A F F Q L Y * T T S A I F
     CSSWGSTPFSSSTRPQVPFL
       V Q A G A V R L F P A L L D H K C H F *
29341 - GAGGTGTTCACGTGCCTCCGATAGGGCCTCTTCCACAGAGTCCCCGAAGCCACGCACTAG - 29400
    -EVFTCLR * GLFHRVPEATH *
    - R C S R A S D R A S S T E S P K P R T S
       G V H V P P I G P L P Q S P R S H A L A
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29401 - CACGTCTCTAACCTGAAGGACAGGCAAACTGAGTTGGACGTGTGTTTTCTCGTTGACACC - 29460
    - H V S N L K D R Q T E L D V C F L V D T
    - T S L T * R T G K L S W T C V F S L T P - R L * P E G Q A N * V G R V F S R * H Q
29461 - AAGAACAAGGCTCTCCATCTTACCTTTCGGTCACACCCGGACGAAACCTAGGTATGCTGA - 29520
    -KNKALHLTFRSHPDET * VC *
    - R T R L S I L P F G H T R T K P R Y A D
    - EQGSPSYLSVTPGRNLGMLM
29521 - TGATCGACTGCAACACGGACGAAACCGTAAGCAGTCTGCAGAAGAGGGACGAGTTACTCG - 29580
    - * S T A T R T K P * A V C R R G T S Y S
    - D R L Q H G R N R K Q S A E E G R V T R
    - I D C N T D E T V S S L Q K R D E L L V
29581 - TTTCTTGTCAACGACAGTAAAATTTATTGTTTATACTGCGTAGGTGCACTAGGCATG - 29640
    -FLVNDSKIYYCLYCVGALGM
    - F L S T T V K F I I V Y T A * V H * A C
     SCQRQ*NLLLFILRRCTRHA
29641 - CAGCCGAGCGACAGCTACACAGATTTTAAAGTTCGTTTAGAGAACAGATCTACAAGAGAT - 29700
    -QPSDSYTDFKVRLENRSTRD
    - S R A T A T Q I L K F V * R T D L Q E I
      AERQLHRF * S S F R E Q I Y K R S
29701 - CGAGGTTGGCTTTTCCTGGGTAGGTAAAAACCTAATAT - 29742
    -RGWLAFPG*VKT*YX
    - E V G W L F L G R * K P N X
    - RLVGFSWVGKNLIX
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FIG. 12 Con't

N-gene primers (nucleotide position 29247-29410) 150# (5'-gactgatgaagctcaggcctt-3') 200# (5'-cttgtgtggtcatcatgagtg-3')

S-gene primers (nucleotide position 24751-25049)
131# (5'-cacagaggaacttctttt-3')
132# (5'-tcccaattcttgaaggtcaatgag-3')

FIG. 13

ATGTCTGATAATGGACCCCAATCAAACCAACGTAGTGCCCCCCGCATTACATTTGGTGGA CCCACAGATTCAACTGACAATAACCAGAATGGAGGACGCAATGGGGCCAAAACAG GGCAAGGAGGAACTTAGATTCCCTCGAGGCCAGGGCGTTCCAATCAACACCAATAGTGGT CCAGATGACCAAATTGGCTACTACCGAAGAGCTACCCGACGAGTTCGTGGTGACGGC AAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCT TCACTTCCCTACGGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTG AATACACCCAAAGACCACATTGGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTA CAACTTCCTCAAGGAACAACATTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGC AGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCT GGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGGAGGTGGTGAAACTGCCCTC GCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAA CAACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGC CAAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCA GAACAAACCCAAGGAAATTTCGGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAA CATTGGCCGCAAATTGCACAATTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGC ATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTG GATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCA TACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCT CAGCCTTTGCCGCAGAGACAAAAGAAGCCCCACTGTGACTCTTCTTCCTGCGGCTGAC ATGGATGATTTCTCCAGACAACTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACT CAGGCATAA

FIG. 14A

MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNTASWFTALTQH
GKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFYYLGTGPEA
SLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVLQLPQGTTLPKGFYAEGSRGG
SQASSRSSSRSRGNSRNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVSGKGQ
QQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYK
HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDA
YKTFPPTEPKKDKKKKKTDEAQPLPQRQKKQPTVTLLPAADMDDFSRQLQNSMSGASADST
QA

FIG. 14B

ATGTTTATTTTCTTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCACCACTTT TGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGGGGGGTTTACTATCCTG GTTACAGGGTTTCATACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTAAGGATGGTAT TTATTTTGCTGCCACAGAGAATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACA ACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTT GAATTGTGTGACAACCCTTTCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGAT ATTCGATAATGCATTTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAG AAAAGTCAGGTAATTTTAAACACTTACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTAT GTTTATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAA ACCTATTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTT CACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTTGGCTATTTAAAGCCAACT ACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAAAATCC ACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCTA ATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACAAACTTGTGTCCTTTT GGAGAGGTTTTTAATGCTACTAAATTCCCTTCTGTCTATGCATGGGAGAGAAAAAAATTTCTAA TTGTGTTGCTGATTACTCTGTGCTCTACAACTCAACATTTTTTTCAACCTTTAAGTGCTATGGCG TTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAG GGAGATGATGTAAGACAAATAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATT GCCAGATGATTTCATGGGTTGTGTCCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTG TCTAATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGCC ATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTAC TTTCTTTTGAACTTTTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCACTGACCTTATT AAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTGTTAACTCCTTCTTC AAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGATTTCACTGATTCCGTTCGAG ATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCTCTTTTGGGGGTGTAAGTGTAATTACA CCTGGAACAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACTGATGTTTC TACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTCTACTGGAAACAATGTAT

TCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATT CCTATTGGAGCTGGCATTTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAA ATCTATTGTGGCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCA TTGCTATACCTACTAACTTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAA ACCTCCGTAGATTGTAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCA ATATGGTAGCTTTTGCACACAACTAAATCGTGCACTCTCAGGTATTGCTGCTGAACAGGATCGCA ACACACGTGAAGTGTTCGCTCAAGTCAAACAAATGTACAAAACCCCAACTTTGAAATATTTTGGT GGTTTTAATTTTCACAAATATTACCTGACCCTCTAAAGCCAACTAAGAGGTCTTTTATTGAGGA CTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAGCAATATGGCGAATGCCTAG GTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTACAGTGTTGCCACCT ATGGACATTTGGTGCTGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATAGGTTCA AAGGCGATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGA CGTTGTTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTG CAATTTCAAGTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATT GACAGGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGGC TGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAAT CAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAGCAGCCCCGCAT GGTGTTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGAGAGGAACTTCACCACAGCGCCAGC AATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTTTTGTGTTTAATGGCACTTCTT GGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAATTACTACAGACAATACATTTGTCTCA GGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTATGATCCTCTGCAACCTGAGCT TGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCACCAGATGTTGATCTTG GCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAG GTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATAT TAAATGGCCTTGGTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAA TCTTGCTTGTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGC TGCAAGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAA

FIG. 15A Con't

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL PFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSOSVIIINNS TNVVIRACNFELCDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK HLREFVFKNKDGFLYVYKGYOPIDVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSP AQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIY QTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTF FSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVROIAPGOTGVIADYNYKLPDDFMGCV LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLND YGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTP SSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQD VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAOVKOMYKTPTLKYFG GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAOKFNGL TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTONVLYE NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN DILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGOSK RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT

FIG. 15B

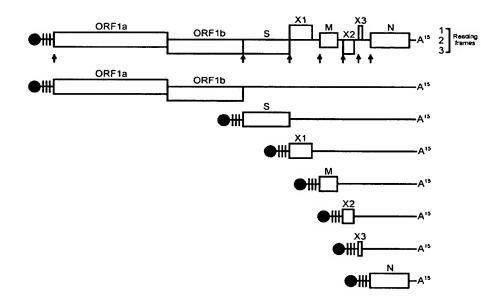


FIG. 16

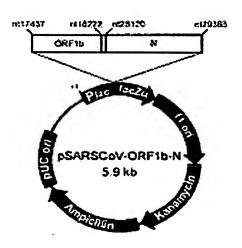


FIG. 17



FIG. 18

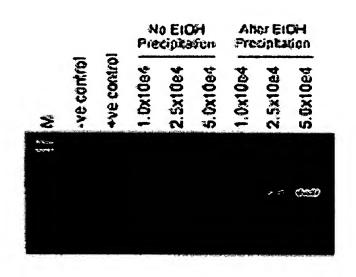


FIG. 19

 Primers for a 225-bp fragment of the region of N-gene that showed no homology to other coronavirus: SRS251: 5'-GCAGTCAAGCCTCTTCTCG-3' (SEQ ID NO:2480) SRS252: 5'-GCCTCAGCAGCAGATTTC-3' (SEQ ID NO:2481)

Primers for 181-bp fragment of the region of 1b-gene:

coro3: 5'-TACACACCTCAGCGTTG-3' (SEQ ID NO:3)

coro4: 5'- CACGAACGTGACGAAT-3' (SEQ ID NO:4)

Primers for a 745-bp fragment from pig β-actin gene:

Actin-F: 5'-TGAGACCTTCAACACGCC-3' (SEQ ID NO:2482) Actin-R: 5'-ATCTGCTGGAAGGTGGAC-3' (SEQ ID NO:2483)

FIG. 20

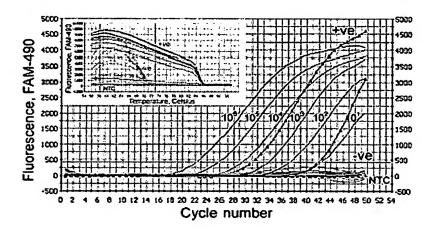


FIG. 21A

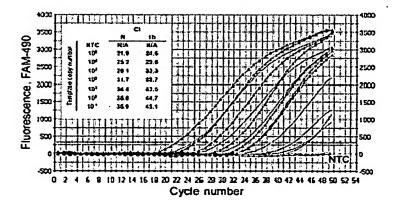


FIG. 21B

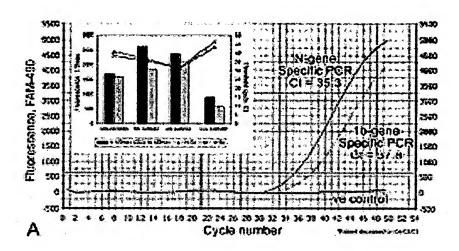


FIG. 22A

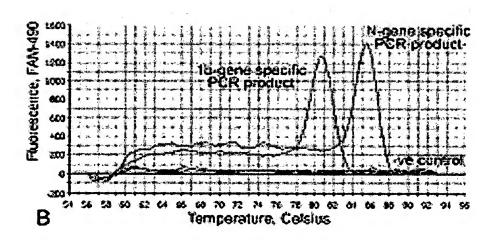


FIG. 22B

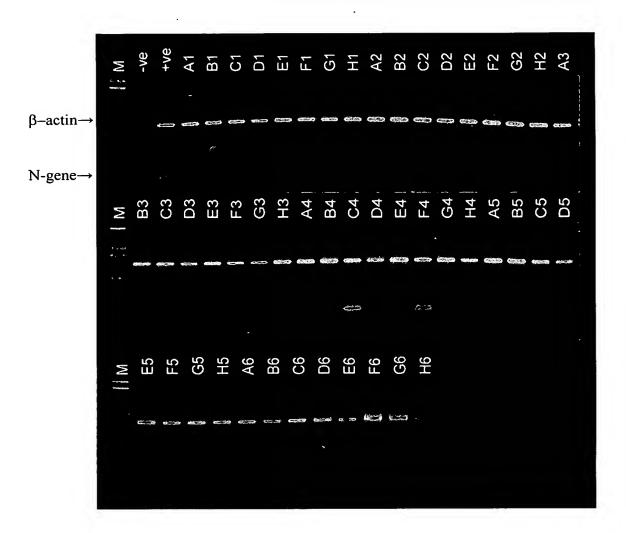


FIG. 23

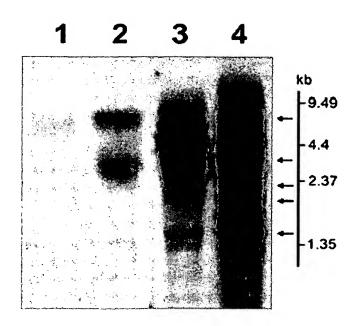


FIG. 24

Sequence	gatataaaattcaagactgaaggattatgtgttgacataccaggcataccaaaggacat gacctaccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatggttac cctaatatgtttatcacccgcgaagaagctattcgtcacgttcgtg	catgggtacacagacacatactatgatattcgataatgcatttaattgcactttcgagtacatatctgatgatgctttcgagtacatttcgagtacattttaaacacttacgagagttttgtgtttaaaaaataaagatggtttctctatgtttataagggctatcaacctatagatgtag	gctgtgacattaaggacctgccaaaagagatcactgtgggctacatcacgaacgctttctt attacaaattaggagcgtcgcagcgtgtaggcactgattcaggttttgctgcatacaacc gctaccgtat	gcagtcaagcctcttctcgctcctcatcacgtagtcgcggtaattcaagaaattcaactc ctggcagcagtaggggaaattctcctgctcgaatggctagcgggggggg
SEQ ID NO	2484	2485	2486	2487
Region	18057 – 18222	21920 – 22107	26867 – 26996	28658 – 28883
Probe	116	S	N	Z

FIG. 25